

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2004, 05:07:05 ; Search time 26244 Seconds
(without alignments)
11757.556 Million cell updates/sec

Title: US-10-005-338B-1
Perfect score: 6525
Sequence: 1 aaatgtgatattttctct.....ttgatcataaagtgaat 6525

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_pa.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_ov.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pi.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6524	100.0	6525	6	AX473847
2	6524	100.0	6525	9	AY028897 Homo sapi
3	6122.8	93.8	6369	6	AX392931 Sequence
4	5373.2	82.3	5475	6	AX537473 Sequence
5	5255.8	80.5	5463	6	AX537470 Sequence
6	5247.4	80.4	5262	6	AX417828 Sequence
7	5039	77.2	5096	9	HGA275973
8	4918.4	75.4	4929	6	AX417824
9	4807.4	73.7	4917	6	AX537472
10	4754.8	72.9	4785	6	AX417826
11	3887	59.6	5347	10	AF491842 Mus muscu
12	3877	59.4	5170	10	RNC426052
13	3868.8	59.3	4929	10	AB097675 Mus muscu
14	3816.2	58.5	4945	10	AB097675 Rattus no
15	3811.6	58.4	4078	9	HSM806823
16	3491	53.5	4664	10	BC064823 Homo sapi
17	3258.2	49.9	3347	6	AX833036
18	3258.2	49.9	3347	6	AX094416 Homo sapi
19	3178	48.7	3268	6	AX714300 Sequence

20	3178	48.7	3268	9	AK056533
21	2795.2	42.8	3112	9	AB067475 Homo sapi
22	2773.6	42.5	2845	9	HS4512612 Homo sapi
23	2591.4	39.7	5243	9	HSM807592
24	1809.4	27.7	2325	6	AX780218 Sequence
25	1808.2	27.7	1964	9	AX122803 Homo sapi
26	1743	26.7	3324	9	HSM808688
27	1731.8	26.5	1943	6	AX834300
28	1731.8	26.5	1943	9	AX096664
29	1722.8	26.4	1818	6	AX576092
30	1685.4	25.8	1700	9	BC070126 Homo sapi
31	1560	23.9	1560	9	AK058170
32	1482	22.9	4921	10	AK129463 Mus muscu
33	1482	18.1	1346	6	AX331591 Sequence
34	1482	18.1	1346	6	AX332287 Sequence
35	1482	18.1	1346	6	AX410760 Sequence
36	1150.4	17.6	6181	6	AX473850
37	1150.4	17.6	6181	9	AY028900
38	1149.8	17.6	5722	6	AX657703 Sequence
39	1149.8	17.6	6333	9	AX247065
40	1123.6	17.2	4875	9	AF423307
41	1118.8	17.1	5981	9	AY028899
42	1118.8	17.1	160254	2	AC007763
43	1118.4	17.1	163229	9	AC115085
44	1118.4	17.1	163229	9	AC115085
45	1118.4	17.1	172223	2	AC115985

ALIGNMENTS

RESULT 1
AX473847

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

location/Qualifiers

1..6525

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match

Best Local Similarity

Matches 6525;

Conservative

Mismatches

Indels

Gaps

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

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0;

Qy	181	CTGTCGTGTTAGTT	CAGTTTCTCAAGCCTTTGTGTCACTAATAGAGATTGGATTATGATG	240
Db	181	CTGTCGTGTTAGTT	CAGTTTCTCAAGCCTTTGTGTCACTAATAGAGATTGGATTATGATG	240
Qy	241	TCCAGCTTGGGAATAT	TACAGGAATTAARAAACAACATTTTTAGAGTGCCTTTCCTGAGCTC	300
Db	241	TCCAGCTTGGGAATAT	TACAGGAATTAARAAACAACATTTTTAGAGTGCCTTTCCTGAGCTC	300
Qy	301	TCCTTCTATTGTT	CCCCCTTCTACTATTTTGTCTCCCTGTGGCTGCTGTTTCTATATCCTCC	360
Db	301	TCCTTCTATTGTT	CCCCCTTCTACTATTTTGTCTCCCTGTGGCTGCTGTTTCTATATCCTCC	360
Qy	361	AGCCAGAGAGCTAGTGTT	ATTTTTCTCCATTGTGTTTACACACTTGTGCAGCTGCAACCCAC	420
Db	361	AGCCAGAGAGCTAGTGTT	ATTTTTCTCCATTGTGTTTACACACTTGTGCAGCTGCAACCCAC	420
Qy	421	CATATCAGGGCCCCAAT	GTAGGAGGTAGACAAGAAAAGCAAAAGGATTTGGCCTCATCC	480
Db	421	CATATCAGGGCCCCAAT	GTAGGAGGTAGACAAGAAAAGCAAAAGGATTTGGCCTCATCC	480
Qy	481	TCTTACAACGATAGTT	CGATTGAATAGAGAGAAAGGTTTTCTCGCTCAGAGTGTGGCT	540
Db	481	TCTTACAACGATAGTT	CGATTGAATAGAGAGAAAGGTTTTCTCGCTCAGAGTGTGGCT	540
Qy	541	GCACCTAGGCTTTTGT	TACTGTAGTCTGGCCCTGTTTACATGGGATTTGTTGCATGTGGGG	600
Db	541	GCACCTAGGCTTTTGT	TACTGTAGTCTGGCCCTGTTTACATGGGATTTGTTGCATGTGGGG	600
Qy	601	ATACAGGAGAAATC	CAGAAAAGAAATTTGCTATTTCTCATTTCTCCCTGAGCATT	660
Db	601	ATACAGGAGAAATC	CAGAAAAGAAATTTGCTATTTCTCATTTCTCCCTGAGCATT	660
Qy	661	AAGACCTCCCTTGC	CTATTCCTCAATCAAGCTTAAGCTTCTTCTGGAGCTGCTCTGT	720
Db	661	AAGACCTCCCTTGC	CTATTCCTCAATCAAGCTTAAGCTTCTTCTGGAGCTGCTCTGT	720
Qy	721	GGGCGGTTCCGGGAGAT	ACCAAGAGAGAAAAGTACCACGTGTTGATATGGTGGTATTTCAA	780
Db	721	GGGCGGTTCCGGGAGAT	ACCAAGAGAGAAAAGTACCACGTGTTGATATGGTGGTATTTCAA	780
Qy	781	ATTTCTGGCTAC	CCCTATTTCACATGCCCTGTTTACTTTTCAGAGCTCAGAGATTGCTGCT	840
Db	781	ATTTCTGGCTAC	CCCTATTTCACATGCCCTGTTTACTTTTCAGAGCTCAGAGATTGCTGCT	840
Qy	841	CCATGCATTTCTGT	CCAGCTTTCCTTAAGAGAGACAGCTTGGAGTATGCTTTAATCCATCTTAC	900
Db	841	CCATGCATTTCTGT	CCAGCTTTCCTTAAGAGAGACAGCTTGGAGTATGCTTTAATCCATCTTAC	900
Qy	901	CTGGGACTGAACA	AGCTGCTTATTTTGGCGHTTAAAAATTACATGCAGTTTACTCGCGTGGC	960
Db	901	CTGGGACTGAACA	AGCTGCTTATTTTGGCGHTTAAAAATTACATGCAGTTTACTCGCGTGGC	960
Qy	961	TCCGGGTTTGTGTT	TTGTTTTCTCTTTAATAGGTTTATTCAGAAAAACATGTCACCTG	1020
Db	961	TCCGGGTTTGTGTT	TTGTTTTCTCTTTAATAGGTTTATTCAGAAAAACATGTCACCTG	1020
Qy	1021	CAATTAGGAGGTAG	GAGTTTGGAGACAGACAGACTTCTACTGAGAAATTACTTTAA	1080
Db	1021	CAATTAGGAGGTAG	GAGTTTGGAGACAGACAGACTTCTACTGAGAAATTACTTTAA	1080
Qy	1081	TTAATCAGAAACCA	AAAGAGTAGTGTTCAGGAAATTTCTTTTTCCACTATTTTTTTTAT	1140
Db	1081	TTAATCAGAAACCA	AAAGAGTAGTGTTCAGGAAATTTCTTTTTCCACTATTTTTTTTAT	1140
Qy	1141	TTTCGGTTAATTAAT	TAGCATGATGCATCCAAATAAGAAATATGAAGAAGTGCTTAATA	1200
Db	1141	TTTCGGTTAATTAAT	TAGCATGATGCATCCAAATAAGAAATATGAAGAAGTGCTTAATA	1200
Qy	1201	TAGAACTCAATCC	TATGGACAGTTTACTCTTTCTAATCTTAATTTCTTGGATATACTCCAG	1260
Db	1201	TAGAACTCAATCC	TATGGACAGTTTACTCTTTCTAATCTTAATTTCTTGGATATACTCCAG	1260
Qy	1261	TGACTAATATTTACA	AGCAGCATCATGACAGAAAGGTGTCCTACTGTGATCACTCACTGATGCA	1320

1261	Db	TGACTTAATATTCAAGCAGCATCATCGAGAAAGTGCTACTGATCAATCTACCTGATGTCA	1320
1321	Qy	TAAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTCTCTAAAGCCGA	1380
1321	Db	TAAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTCTCTAAAGCCGA	1380
1381	Qy	GCAACTTTGTAGTGTGGTTTTTCAAGAGATCCAGTGTCTTATGAACTTCGTTTTTTTTTCCCTG	1440
1381	Db	GCAACTTTGTAGTGTGGTTTTTCAAGAGATCCAGTGTCTTATGAACTTCGTTTTTTTTTCCCTG	1440
1441	Qy	ATATGATTCAGATATCTTCTATTTATATGAGTAATCAAGAGCTGGCTGTTCAAAATCATGTG	1500
1441	Db	ATATGATTCAGATATCTTCTATTTATATGAGTAATCAAGAGCTGGCTGTTCAAAATCATGTG	1500
1501	Qy	AGCGTCTCAGTACTGGTCTCTCAGGTTTCACAGTTTTCACAGCATCCATAGATGCTGCCA	1560
1501	Db	AGCGTCTCAGTACTGGTCTCTCAGGTTTTCACAGTTTTCACAGCATCCATAGATGCTGCCA	1560
1561	Qy	TTATACAGTTGAAGACCAATGTTTCTCTTTGGAAAGAGCTGGAGTCAACTTAAAGCTGTTTA	1620
1561	Db	TTATACAGTTGAAGACCAATGTTTCTCTTTGGAAAGAGCTGGAGTCAACTTAAAGCTGTTTA	1620
1621	Qy	TTATGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCGCCGAGAGTAATTTTAAATAT	1680
1621	Db	TTATGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCGCCGAGAGTAATTTTAAATAT	1680
1681	Qy	ACCTAGTTATAGCATTTTCACCTTTTGGATACATTTTGGCAATTCATATCGTAGCAGAAA	1740
1681	Db	ACCTAGTTATAGCATTTTCACCTTTTGGATACATTTTGGCAATTCATATCGTAGCAGAAA	1740
1741	Qy	AAGAAAAAATAAAGAAATTTTAAAGATAATGGGACHTTCATGATCTGCCTTTTGGC	1800
1741	Db	AAGAAAAAATAAAGAAATTTTAAAGATAATGGGACHTTCATGATCTGCCTTTTGGC	1800
1801	Qy	TTTCTCTGGGTTCTTCTATATACAGGTTTAAATTTTCTATGTCCTTCTATGCGCAGTCA	1860
1801	Db	TTTCTCTGGGTTCTTCTATATACAGGTTTAAATTTTCTATGTCCTTCTATGCGCAGTCA	1860
1861	Qy	TTGCGACAGCTTCTTTGTTATTTTCCCTCAAGTAGCAGCATTTGTGATTTTCTGCTTTTTT	1920
1861	Db	TTGCGACAGCTTCTTTGTTATTTTCCCTCAAGTAGCAGCATTTGTGATTTTCTGCTTTTTT	1920
1921	Qy	TCCTTTATGGAATTATCATCTGTAATTTTGGCTTTTAAATGCTGACACCTCTTTTAAAAAAT	1980
1921	Db	TCCTTTATGGAATTATCATCTGTAATTTTGGCTTTTAAATGCTGACACCTCTTTTAAAAAAT	1980
1981	Qy	CAAAAACATGTGGGAATAGTTGAATTTTGTACTGTCGGCTTTTGGATTTATTTGGCCTTA	2040
1981	Db	CAAAAACATGTGGGAATAGTTGAATTTTGTACTGTCGGCTTTTGGATTTATTTGGCCTTA	2040
2041	Qy	TGATAATCTCTCATAGAAAGTTTTTCCAAATCGTTTAGTGTGGCTTTTCAGTCCCTTCTGTG	2100
2041	Db	TGATAATCTCTCATAGAAAGTTTTTCCAAATCGTTTAGTGTGGCTTTTCAGTCCCTTCTGTG	2100
2101	Qy	ACTGTACTTTTGTGATTTGATTTGCACAGTCAATGATTTAGAAAGATTTTAAATGAAGGTG	2160
2101	Db	ACTGTACTTTTGTGATTTGATTTGCACAGTCAATGATTTAGAAAGATTTTAAATGAAGGTG	2160
2161	Qy	CTTCAATTTCAAATTTGACTGCGAGGCCCATATCCTCTAAATTTATTAATTTATCATGCTCA	2220
2161	Db	CTTCAATTTCAAATTTGACTGCGAGGCCCATATCCTCTAAATTTATTAATTTATCATGCTCA	2220
2221	Qy	CAGTTAATAGTATATCTATGTCCTCTGCTCTCTATCTTGATCAAGTCATTTCCAGGGG	2280
2221	Db	CAGTTAATAGTATATCTATGTCCTCTGCTCTCTATCTTGATCAAGTCATTTCCAGGGG	2280
2281	Qy	AAATTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCCATATTTGGTCAAGAGTA	2340
2281	Db	AAATTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCCATATTTGGTCAAGAGTA	2340
2341	Qy	AAGAAATATGAGGAGTTATCAGAGGCCAATGTTTAAATGGAATATATAGTTTATAGTGAAA	2400

Db	2341	AAAGAAATTAAGAGAGTTATACAGAGGCAATGTTAAATGGAAATATAGTTTTAGTGAAA	2400
Qy	2401	TTATTGAGCCAGTTTCTTTCAGAAATTTGTAGAAAAGAACCAATAGAAATTAGTGGTATTC	2460
Db	2401	TTATTGAGCCAGTTTCTTTCAGAAATTTGTAGAAAAGAACCAATAGAAATTAGTGGTATTC	2460
Qy	2461	AGAAGACATACAGAAAGAGGGTGAAAATGTGAGAGCTTTGAGAAATTTGTCAATTTGACA	2520
Db	2461	AGAAGACATACAGAAAGAGGGTGAAAATGTGAGAGCTTTGAGAAATTTGTCAATTTGACA	2520
Qy	2521	TATATGAGGGTCAGATTACTTCTGCGCCACAGTGGACAGAGAAAGATACATTGCA	2580
Db	2521	TATATGAGGGTCAGATTACTTCTGCGCCACAGTGGACAGAGAAAGATACATTGCA	2580
Qy	2581	TGAATATCTTTGTGGACTGCGCCACCTTCTGATGGTTTGCATCTATATATGGACACA	2640
Db	2581	TGAATATCTTTGTGGACTGCGCCACCTTCTGATGGTTTGCATCTATATATGGACACA	2640
Qy	2641	GAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAATGATGGCAATTTGTCCACAGT	2700
Db	2641	GAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAATGATGGCAATTTGTCCACAGT	2700
Qy	2701	TAGATATACACTTTGATGTTTTCAGCAGTAGAAGAAATTTATCAATTTTGGCTTCAATCA	2760
Db	2701	TAGATATACACTTTGATGTTTTCAGCAGTAGAAGAAATTTATCAATTTTGGCTTCAATCA	2760
Qy	2761	AAGGGATACAGCCCAACATATATACAGAGTGCAGAGGTTTTACTAGATTTAGACA	2820
Db	2761	AAGGGATACAGCCCAACATATATACAGAGTGCAGAGGTTTTACTAGATTTAGACA	2820
Qy	2821	TGCAGACTATCAAGATPAAACAGTCAAGTAAATAATTAAGTGGTGGTCAAAAAGAAAGCTGT	2880
Db	2821	TGCAGACTATCAAGATPAAACAGTCAAGTAAATAATTAAGTGGTGGTCAAAAAGAAAGCTGT	2880
Qy	2881	CATTAGAAATGCTGTTCTTGGGAAACCAAGATACCTGCTGATAGAAACCAACAGCTG	2940
Db	2881	CATTAGAAATGCTGTTCTTGGGAAACCAAGATACCTGCTGATAGAAACCAACAGCTG	2940
Qy	2941	GAATGGACCCCTGTTCTCGACATATGATGGAAATCTTTTAAATAACAGAAAAGCCAAATC	3000
Db	2941	GAATGGACCCCTGTTCTCGACATATGATGGAAATCTTTTAAATAACAGAAAAGCCAAATC	3000
Qy	3001	GGGTGACAGTGTTCAGTACTCATTTCAATGATGAGCTGACATCTTTCAGATAGGAAAG	3060
Db	3001	GGGTGACAGTGTTCAGTACTCATTTCAATGATGAGCTGACATCTTTCAGATAGGAAAG	3060
Qy	3061	CTGTGATATCAAGAGATGCTGAATGTGTGGTTCTTCAATGTTCTTCAAAAGTAAAT	3120
Db	3061	CTGTGATATCAAGAGATGCTGAATGTGTGGTTCTTCAATGTTCTTCAAAAGTAAAT	3120
Qy	3121	GGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTTGCGCACAGAAATCTCTTT	3180
Db	3121	GGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTTGCGCACAGAAATCTCTTT	3180
Qy	3181	CTTCACTGGTTTAAACACATATACCTGGAGCTACTTTATTACACAGAAATGACCAACAC	3240
Db	3181	CTTCACTGGTTTAAACACATATACCTGGAGCTACTTTATTACACAGAAATGACCAACAC	3240
Qy	3241	TTGTGATAGCTTGCCTTCAAGACATGGACAAATTTTCAGGTTTCTTGGCCCTAG	3300
Db	3241	TTGTGATAGCTTGCCTTCAAGACATGGACAAATTTTCAGGTTTCTTGGCCCTAG	3300
Qy	3301	ACAGTCAATCAAAATTTGGGTGTCATTTCTTATGTTGTTTCCATGACGACTTTGGAAGAG	3360
Db	3301	ACAGTCAATCAAAATTTGGGTGTCATTTCTTATGTTGTTTCCATGACGACTTTGGAAGAG	3360
Qy	3361	TATTTTAAAGCTAGAGTTCAAGCAGAAATTTGACAGAGATTAAGTGTATTTACTC	3420
Db	3361	TATTTTAAAGCTAGAGTTCAAGCAGAAATTTGACAGAGATTAAGTGTATTTACTC	3420
Qy	3421	AGCAGCCACTGGAGGAAGAAATGGAATTCAAAATCTTTTGTAGAAATGGAACAGAGCTTAC	3480
Db	3421	AGCAGCCACTGGAGGAAGAAATGGAATTCAAAATCTTTTGTAGAAATGGAACAGAGCTTAC	3480
Qy	3481	TTATTTCTTCTGAAACCAAGGCTTCTCTAGTGAGACCAATGAGGCTTTGGAAAACACAGA	3540
Db	3481	TTATTTCTTCTGAAACCAAGGCTTCTCTAGTGAGACCAATGAGGCTTTGGAAAACACAGA	3540
Qy	3541	TGTATACAAATAGCAAAAGTTTCAATTTCTTTTACCTTGAACAGTGAAGTAAATCAGTGAGAT	3600
Db	3541	TGTATACAAATAGCAAAAGTTTCAATTTCTTTTACCTTGAACAGTGAAGTAAATCAGTGAGAT	3600
Qy	3601	CAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTTTGTTTCTATC	3660
Db	3601	CAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTTTGTTTCTATC	3660
Qy	3661	ACTCTTTTAAATAATGCTGCTGCTCCCATCAACCTGTTTCCAGACTTATATATTTCTAAAC	3720
Db	3661	ACTCTTTTAAATAATGCTGCTGCTCCCATCAACCTGTTTCCAGACTTATATATTTCTAAAC	3720
Qy	3721	CTGGAGACAAACCAACATAAATACAAAACAGTCTGCTTCTTCAAAATTTCTGCTGACTCAG	3780
Db	3721	CTGGAGACAAACCAACATAAATACAAAACAGTCTGCTTCTTCAAAATTTCTGCTGACTCAG	3780
Qy	3781	ATATCAGTGATCTTATTTAGCTTTTTCACAGCCAGAACATATGTTGACGATGATTATG	3840
Db	3781	ATATCAGTGATCTTATTTAGCTTTTTCACAGCCAGAACATATGTTGACGATGATTATG	3840
Qy	3841	ACAGTGAATCTATCTATCTGCTGCTCCCATAGTGGGCTTTAAATGTTGATGCAATTCAGAAA	3900
Db	3841	ACAGTGAATCTATCTATCTGCTGCTCCCATAGTGGGCTTTAAATGTTGATGCAATTCAGAAA	3900
Qy	3901	AGGACTATGTTTTTTCAGCTGTTTTCACAGTACTATGTTTTCATGCTTATTTTCTTACTATATG	3960
Db	3901	AGGACTATGTTTTTTCAGCTGTTTTCACAGTACTATGTTTTCATGCTTATTTTCTTACTATATG	3960
Qy	3961	TGAATATCATATAGTAACCTACTATCTTATCATTTAAATGTTGATGCAATTCAGAAATG	4020
Db	3961	TGAATATCATATAGTAACCTACTATCTTATCATTTAAATGTTGATGCAATTCAGAAATG	4020
Qy	4021	GGAGTACCCCAATCTTTCAGAAATTTACTGATATAGTTTTTAAATTCAGGCTGATTTTC	4080
Db	4021	GGAGTACCCCAATCTTTCAGAAATTTACTGATATAGTTTTTAAATTCAGGCTGATTTTC	4080
Qy	4081	AAGCAGCTTTGCTTGGAAATCATTTGTTGATGCAATGCCACCTTACTTTGCCATGGAATG	4140
Db	4081	AAGCAGCTTTGCTTGGAAATCATTTGTTGATGCAATGCCACCTTACTTTGCCATGGAATG	4140
Qy	4141	CAGAGAAATCAAGATCAAAAGCTTATCTCAACTTTAAACTTTTCAGGCTTTTGGCATCTG	4200
Db	4141	CAGAGAAATCAAGATCAAAAGCTTATCTCAACTTTAAACTTTTCAGGCTTTTGGCATCTG	4200
Qy	4201	CATATGGATGGACAAGCTGTTGTTGATATCCCTTATTTTATCATTTCTTATTTTGA	4260
Db	4201	CATATGGATGGACAAGCTGTTGTTGATATCCCTTATTTTATCATTTCTTATTTTGA	4260
Qy	4261	TGCTAGGAGCTTACTGGCATTTTATGATTTATTTTATTTTATTTTATTTTATTTTATTTT	4320
Db	4261	TGCTAGGAGCTTACTGGCATTTTATGATTTATTTTATTTTATTTTATTTTATTTTATTTT	4320
Qy	4321	CTGTGTTTTTGGCTTATTTGTTTATGTTTCCATGATTTCTGTTTCTTATTTATTTGCTT	4380
Db	4321	CTGTGTTTTTGGCTTATTTGTTTATGTTTCCATGATTTCTGTTTCTTATTTATTTGCTT	4380
Qy	4381	CTTTTCACTTTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCAATTTATCTTCTGTGG	4440
Db	4381	CTTTTCACTTTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCAATTTATCTTCTGTGG	4440
Qy	4441	CAGCGTTGCTTGTATTTGCAATCACTGAAATTAACCTTTCTTTATGGGATACACAATTCGAA	4500
Db	4441	CAGCGTTGCTTGTATTTGCAATCACTGAAATTAACCTTTCTTTATGGGATACACAATTCGAA	4500
Qy	4501	CTATTTCTTCAATATGCTTTTGTATCATCATTTCCAAATCTTCACTTCTAGGTTGCTTGA	4560
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4561 TTTCTTTTCATAGAATTTCTTGGAAAGAAATGTACGAAAAAATGTGGACACCTTATAATCCAT 4620
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4621 GGGATAGGCTTTCACTAGTGTATATCGCCTTACTCTGAGTGTACTGTGGATTTTCC 4680
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5161 CTTTGTGGCCAGATCTACATTTGAGGAAACATTTTGAATTTATGGAGCTGTCAAGGAA 5220
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5401 ATCCCAAGCCAAACAGACATGTGGCGAGCAATTTGAACTGCAATTTAAAAACGAAAGC 5460
5401 ATCCCAAGCCAAACAGACATGTGGCGAGCAATTTGAACTGCAATTTAAAAACGAAAGC 5460
5461 GGGCTGCTATCTGACCACTCACTATAAGGAGAGGAGAGGCTGTCTGTGATGAGTAG 5520
5461 GGGCTGCTATCTGACCACTCACTATAAGGAGAGGAGAGGCTGTCTGTGATGAGTAG 5520
5521 CTATCATGTGTCTGGGCAAGTAAAGATGTATCGGAAACAGTACAACTCTAAAGAGTAAAT 5580
5521 CTATCATGTGTCTGGGCAAGTAAAGATGTATCGGAAACAGTACAACTCTAAAGAGTAAAT 5580
5581 TTGGAAGAGGCTACTTTTGGAAATTTAAATTTGAAGAGCTGGATAGAAAAACCTTAGAAGTAG 5640
5581 TTGGAAGAGGCTACTTTTGGAAATTTAAATTTGAAGAGCTGGATAGAAAAACCTTAGAAGTAG 5640
5641 ACCGCTTCAAGAGAAATTCAGTATATTTTCCAAATGCAAGCCGTGAGGAAAGTTTTT 5700

Db 5641 ACCGCTTCAAGAGAAATTCAGTATATTTTCCAAATGCAAGCCGTGAGGAAAGTTTTT 5700
QY 5701 CTTCTATTTTGGCTTATAAAATTCCTAAGAAAGATGTTTCAGTCCCTTTTACAAATCTTTT 5760
Db 5701 CTTCTATTTTGGCTTATAAAATTCCTAAGAAAGATGTTTCAGTCCCTTTTACAAATCTTTT 5760
QY 5761 TTAAGCTGAAAGAACTAAACATGCTTTTGGCAATTAAGAAATATAGCTTTTCTCAAGCAA 5820
Db 5761 TTAAGCTGAAAGAACTAAACATGCTTTTGGCAATTAAGAAATATAGCTTTTCTCAAGCAA 5820
QY 5821 CATTTGAAACAGGTTTTTGTAGAACTCCTAAAGAAACAGAGGAGAAATAGTGTG 5880
Db 5821 CATTTGAAACAGGTTTTTGTAGAACTCCTAAAGAAACAGAGGAGAAATAGTGTG 5880
QY 5881 GAACTTTAAACAGCACACTTTTGGTGGAAACGAAACCAAGAGATAGAGTAGTATTTTGAA 5940
Db 5881 GAACTTTAAACAGCACACTTTTGGTGGAAACGAAACCAAGAGATAGAGTAGTATTTTGAA 5940
QY 5941 TTTGTATTTCTCGTCTGCTTACTGGGACTTCTTTCTTTTTCACTTAAATTTTAACTTTGG 6000
Db 5941 TTTGTATTTCTCGTCTGCTTACTGGGACTTCTTTCTTTTTCACTTAAATTTTAACTTTGG 6000
QY 6001 TTTTAAAGAGTTTTTATTTGGAATGTAATCTGGAGAAACCAAGAAACGCACTTGAAATTTTC 6060
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QY 6061 TAAGCTCCTTAATTAAGTGAATGCTGTGGTGTGTTTGTCTTTTCTTAAATAAAGCTAT 6120
Db 6061 TAAGCTCCTTAATTAAGTGAATGCTGTGGTGTGTTTGTCTTTTCTTAAATAAAGCTAT 6120
QY 6121 GTATAATTAAGTGAAGCTGCACTGTTTGTATTTGAAGTATATTTGAAGTATATAGTATTG 6180
Db 6121 GTATAATTAAGTGAAGCTGCACTGTTTGTATTTGAAGTATATTTGAAGTATATAGTATTG 6180
QY 6181 TCATCTTTTTCACCATTCAGAAACAGTGTCTTGAATTTGTGATTTAAGGAATTTGTAAT 6240
Db 6181 TCATCTTTTTCACCATTCAGAAACAGTGTCTTGAATTTGTGATTTAAGGAATTTGTAAT 6240
QY 6241 AGAATAGTTTTTATTTTAAAGTTATCTTTAAAGTTTATGTCATCTTCTTAAATAAGTACGTA 6300
Db 6241 AGAATAGTTTTTATTTTAAAGTTATCTTTAAAGTTTATGTCATCTTCTTAAATAAGTACGTA 6300
QY 6301 ATGTTCCCAATCTAAATFAAAAAAATAATACATACTAATACTAATGCATAGAAAAAGATACATAAGC 6360
Db 6301 ATGTTCCCAATCTAAATFAAAAAAATAATACATACTAATACTAATGCATAGAAAAAGATACATAAGC 6360
QY 6361 AATGTCAAGAGTTTTCTGCTCTCTCTTTTAAATTTCTTAAAAAGCCACTTTTGAATGGAAGT 6420
Db 6361 AATGTCAAGAGTTTTCTGCTCTCTCTTTTAAATTTCTTAAAAAGCCACTTTTGAATGGAAGT 6420
QY 6421 TGTCAATCCCGTAAAGCTGAAAGTGTAAAGCTAGTAAAGTCTCAATATAGAGATTGAGGAA 6480
Db 6421 TGTCAATCCCGTAAAGCTGAAAGTGTAAAGCTAGTAAAGTCTCAATATAGAGATTGAGGAA 6480
QY 6481 AGTTATATCCACTAGTGGCAGTGTATGATCATATTAAGTGAAT 6525
Db 6481 AGTTATATCCACTAGTGGCAGTGTATGATCATATTAAGTGAAT 6525

RESULT 2

AY028897 Homo sapiens ATP-binding cassette A5 mRNA, complete cds. PRI 01-DEC-2001
LOCUS AY028897
DEFINITION Homo sapiens ATP-binding cassette A5 mRNA, complete cds.
ACCESSION AY028897
VERSION AY028897.1 GI:17223619
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 6525)
AUTHORS Schriml, L.M., Arnould, I., Prades, C., Lachtermacher-Rocha, M.,

Qy	1261	TGACTAATATTCAAGCAGCATCATGCGAGAAAGTGTTCTACTGATCATCTACCTGATGTCA	1320
Db	1261	TGACTAATATTCAAGCAGCATCATGCGAGAAAGTGTTCTACTGATCATCTACCTGATGTCA	1320
Qy	1321	TAATTAAGTGAAGAAATATACAAATGAAAGAAATGTTAAACATCCAGTCTCTTAAGCCGA	1380
Db	1321	TAATTAAGTGAAGAAATATACAAATGAAAGAAATGTTAAACATCCAGTCTCTTAAGCCGA	1380
Qy	1381	GCAACTTTGAGGTGGTTTTCAAGACATCCATGCTCTATGAACCTTCGTTTTTTTCCCTG	1440
Db	1381	GCAACTTTGAGGTGGTTTTCAAGACATCCATGCTCTATGAACCTTCGTTTTTTTCCCTG	1440
Qy	1441	ATATGATTCAGTATCTTCTATTATATGGAATCAAGAGCTGCTGTTCAAAATCATGTG	1500
Db	1441	ATATGATTCAGTATCTTCTATTATATGGAATCAAGAGCTGCTGTTCAAAATCATGTG	1500
Qy	1501	AGGCTGCTCAGTACTGCTCAGGTTTCACAGTTTACAGCATCCATAGATGCTGCCTCA	1560
Db	1501	AGGCTGCTCAGTACTGCTCAGGTTTCACAGTTTACAGCATCCATAGATGCTGCCTCA	1560
Qy	1561	TTATACAGTTCAAGACCAATGTTTCTCTTTGGAAGAGCTGGAGTCAACTAAAGCTGTTA	1620
Db	1561	TTATACAGTTCAAGACCAATGTTTCTCTTTGGAAGAGCTGGAGTCAACTAAAGCTGTTA	1620
Qy	1621	TTATGGAGAAAATGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTAATTTTAATAT	1680
Db	1621	TTATGGAGAAAATGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTAATTTTAATAT	1680
Qy	1681	ACCTAGTTATAGCAATTTTCACTTTTGGAATATTTTGGCAATTCATATCGTAGCAGAAA	1740
Db	1681	ACCTAGTTATAGCAATTTTCACTTTTGGAATATTTTGGCAATTCATATCGTAGCAGAAA	1740
Qy	1741	AAGAAAAAAATTAAGAAATTTTAAAGATAATGGGACTTCATGATCTGCTTTTGGC	1800
Db	1741	AAGAAAAAAATTAAGAAATTTTAAAGATAATGGGACTTCATGATCTGCTTTTGGC	1800
Qy	1801	TTTCTCGGTTCTCTATATACAGTTTAAATTTTCTATGTCCTCTCTTATGGCAGTCA	1860
Db	1801	TTTCTCGGTTCTCTATATACAGTTTAAATTTTCTATGTCCTCTCTTATGGCAGTCA	1860
Qy	1861	TTGCGACAGCTCTTTGTTATTTCTCAAAGTAGCAGCATTTGATATTTCTGCTTTT	1920
Db	1861	TTGCGACAGCTCTTTGTTATTTCTCAAAGTAGCAGCATTTGATATTTCTGCTTTT	1920
Qy	1921	TCCTTTATGATATATCATCTGTATTTTCTTTTAAATGCTTGAACCTCTTTTAAAAAAT	1980
Db	1921	TCCTTTATGATATATCATCTGTATTTTCTTTTAAATGCTTGAACCTCTTTTAAAAAAT	1980
Qy	1981	CAAAACATGCGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATTTATTTGGCCTTA	2040
Db	1981	CAAAACATGCGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATTTATTTGGCCTTA	2040
Qy	2041	TGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCAGTCCCTTCGTC	2100
Db	2041	TGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCAGTCCCTTCGTC	2100
Qy	2101	ACTGTACTTTGATTTGGTATTCACAGAGTCATGCAATTTAGAAATTTTAAATGAAGGTG	2160
Db	2101	ACTGTACTTTGATTTGGTATTTGCAAGGTGATGCAATTTAGAAATTTTAAATGAAGGTG	2160
Qy	2161	CTTCATTTTCAAAATTTGAGCTGCAGGCCCATATCTCTTAATTTATCAATTTATCATGCTCA	2220
Db	2161	CTTCATTTTCAAAATTTGAGCTGCAGGCCCATATCTCTTAATTTATCAATTTATCATGCTCA	2220
Qy	2221	CACTTAATAGTATATCTATGTCTCTTGGCTGTCTATCTTTGATCAAGTCAATTCAGGGG	2280
Db	2221	CACTTAATAGTATATCTATGTCTCTTGGCTGTCTATCTTTGATCAAGTCAATTCAGGGG	2280
Qy	2281	AATTTGCTTACGAGATCATCTTTTATTTTCTGAAGCCCTTCATATGCTCAAAAGTGA	2340
Db	2281	AATTTGCTTACGAGATCATCTTTTATTTTCTGAAGCCCTTCATATGCTCAAAAGTGA	2340

Qy	2341	AAAGAAATTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATAGTTTTAGTGA	2400
Db	2341	AAAGAAATTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATAGTTTTAGTGA	2400
Qy	2401	TTATTGAGCCAGTTCTTTCAGAAATTTGTAGGAAAGAACGCATTAAGAAATTAGTGGTATT	2460
Db	2401	TTATTGAGCCAGTTCTTTCAGAAATTTGTAGGAAAGAACGCATTAAGAAATTAGTGGTATT	2460
Qy	2461	AGAAGACATACAGAAAGAGGGTCAAAATGTTGAGGCTTTGAGAAATTTGTCATTTTGACA	2520
Db	2461	AGAAGACATACAGAAAGAGGGTCAAAATGTTGAGGCTTTGAGAAATTTGTCATTTTGACA	2520
Qy	2521	TATATGAGGGTCAGATTACTGCTTACTTGGCCACACAGTGGAAACAGAAAGAGTACATTGA	2580
Db	2521	TATATGAGGGTCAGATTACTGCTTACTTGGCCACACAGTGGAAACAGAAAGAGTACATTGA	2580
Qy	2581	TGAATATTTCTTGTGGACTCTGCCACCTTCTGATGGGTTTGCATCTATATATGGACACA	2640
Db	2581	TGAATATTTCTTGTGGACTCTGCCACCTTCTGATGGGTTTGCATCTATATATGGACACA	2640
Qy	2641	GAGTCTCAGAAATAGATGAAATGTTTGAACACAGAAAAATGATTGGCAATTTGTCCACAGT	2700
Db	2641	GAGTCTCAGAAATAGATGAAATGTTTGAACACAGAAAAATGATTGGCAATTTGTCCACAGT	2700
Qy	2701	TAGATATACACTTTTGATGTTTTCACAGTAGAAGAAAATTTATCAATTTTGGCTTCAATCA	2760
Db	2701	TAGATATACACTTTTGATGTTTTCACAGTAGAAGAAAATTTATCAATTTTGGCTTCAATCA	2760
Qy	2761	AAGGGATACAGGCCAACATATATATACAGAAAGTGCAGAAAGTTTTACTAGATTTAGACA	2820
Db	2761	AAGGGATACAGGCCAACATATATATACAGAAAGTGCAGAAAGTTTTACTAGATTTAGACA	2820
Qy	2821	TGCAGACTATCAAGATATAACCAAGCTTAAAAATTAAGTGGTGGTCAAAAAGAAAGCTGT	2880
Db	2821	TGCAGACTATCAAGATATAACCAAGCTTAAAAATTAAGTGGTGGTCAAAAAGAAAGCTGT	2880
Qy	2881	CATTAGGAATGCTGTTTGGGAACCCAAAGATATGCTGCTAGATGAACCAACAGCTG	2940
Db	2881	CATTAGGAATGCTGTTTGGGAACCCAAAGATATGCTGCTAGATGAACCAACAGCTG	2940
Qy	2941	GAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATACAGAAAAAGCCAATC	3000
Db	2941	GAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATACAGAAAAAGCCAATC	3000
Qy	3001	GGGTGACAGTGTTTCAGTACTCATTTTCATGATGAAGCTGACATTTCTTTCGAGATAGAAAG	3060
Db	3001	GGGTGACAGTGTTTCAGTACTCATTTTCATGATGAAGCTGACATTTCTTTCGAGATAGAAAG	3060
Qy	3061	CTGTGATATACAAAGNATCCTGAAATGTTGGTTCCTCAATGTCCCTCAAAAGTAAAT	3120
Db	3061	CTGTGATATACAAAGNATCCTGAAATGTTGGTTCCTCAATGTCCCTCAAAAGTAAAT	3120
Qy	3121	GGGGGATCGGCTACCGCCTCAGCATGTACATAGACAAATATTGTGCCACAGAAATCTCTTT	3180
Db	3121	GGGGGATCGGCTACCGCCTCAGCATGTACATAGACAAATATTGTGCCACAGAAATCTCTTT	3180
Qy	3181	CTTCACCTGGTTAAACACATATATCTGGAGCTACTTTTATTAACACAGAAATGACCAACAC	3240
Db	3181	CTTCACCTGGTTAAACACATATATCTGGAGCTACTTTTATTAACACAGAAATGACCAACAC	3240
Qy	3241	TTGTGTATAGCTTGCCTTTCAGGACATGACAAAATTTTCAGGCTTTGTTTTCTGCCCTAG	3300
Db	3241	TTGTGTATAGCTTGCCTTTCAGGACATGACAAAATTTTCAGGCTTTGTTTTCTGCCCTAG	3300
Qy	3301	ACAGTCAATCAAAATTTGGGTGTCATTTCTTATGGTGTTCCTCATGACATTTTGGAGACG	3360
Db	3301	ACAGTCAATCAAAATTTGGGTGTCATTTCTTATGGTGTTCCTCATGACATTTTGGAGACG	3360
Qy	3361	TATTTTTAAAGCTAGAGTTGAGCGAATTCACCAAGCAGATTTATAGTGTATTTTACTC	3420
Db	3361	TATTTTTAAAGCTAGAGTTGAGCGAATTTGACCAAGCAGATTTATAGTGTATTTTACTC	3420
Qy	3421	AGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTTTGATGAATGGAAACAGAGCTTAC	3480

3421 AGCAGCCATCGGAGGAGAAATGGATTCAAAATCTTTTGATGAAATGGAAACAGAGCTTAC 3480
3481 TTATCTCTTCTGAAACCAAGGCTTCCTAGTGAGCACCAGTGGCCTTTGGAACACACAGA 3540
3481 TTATCTCTTCTGAAACCAAGGCTTCCTAGTGAGCACCAGTGGCCTTTGGAACACACAGA 3540
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3661 ACTCTTTTAAATATGCTGGTTCCTCATCAAACTTGTTCAGACTTATATTTTCTAAAC 3720
3721 CTGGAGACAAACACATATAAACAAGTCTGCTTCTTCAAAATTTCTGCTGACTCAG 3780
3781 ATATCAGTGATCTTATAGCTTTTCAAAAGCAGACATAATGCTGACGATGATTAATG 3840
3781 ATATCAGTGATCTTATAGCTTTTCAAAAGCAGACATAATGCTGACGATGATTAATG 3840
3841 ACAGTGACTATGATCGTGGCTCCCATAGTGGCGCTTTAAATGTGATGCATTCAGAAA 3900
3901 AGGACTATGTTTGGAGCTGTTTCAACAGTACTATGTTTATCTTTACCTATATTTAG 3960
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4081 AAGCAGCTTTCGTTGGAATCAATGTACTGCAATGCCACCTTACTTTGGCATGGAAAATG 4140
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4381 CTTTTCACCTTTAAGAAATTTTAAATACCAAGAAATTTTGGTCAATTTATCTATCTGTTG 4440
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4621 GGGATAGCTTTTCTAGTACTGTTATATCGCTTACCTGCACTGAGTGTACTGTGGATTTTCC 4680
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4741 GAAACCTTTTCAACGAAGTCTTAAATATAGGAAGCTTCCAGAACCCACAGACAAATGAGATG 4800
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Qy 1008 ATTCTGGTCTACCTATTTTACATGCTGTTTCTTTTACATGCTGACAGATGCTGCT 1067
Qy 841 CCAATGANTCTGCTCCAGTTTCTTAAGAGACAGCTTGGAGTATGCTTAATCCATCTTAC 900
Db
Qy 1068 CCATGCAATCTGCTCCAGTTTCTTAAGAGACAGCTTGGAGTATGCTTAATCCATCTTAC 1127
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Db
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Qy 1741 AAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGACTGCTTTTGGC 1800
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Qy 2028 TTTCTGGGTTCTCTATATACAGTTTAAATTTTCTATGTCCTTTCTATGGCAGTCA 2087
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Db 2088 TTGGACAGCTTCTTTGTTATTTCTCAAGTAGCAGCATTTGATATTTCTGCTTTTTT 2147
Qy 1921 TCCCTTATGGATATCATCTGATTTTCTTTAAATGCTCAGACCTCTTTTAAAAAAT 1980
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Qy 1981 CAAACATGCTGGAAATAGTTGAAATTTTGTATCTGCTGCTTTTGGATTTATGGCCTTA 2040
Db 2208 CAAACATGCTGGAAATAGTTGAAATTTTGTATCTGCTGCTTTTGGATTTATGGCCTTA 2267
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LOCUS
DEFINITION Sequence 4 from Patent WO02070690.
5475 bp DNA linear PAT 23-NOV-2002

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Chen, H., Kilinski, L. and le Bihan, S.
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LOCUS AX537470 5463 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 1 from Patent WO2070690.
ACCESSION AX537470
VERSION AX537470.1 GI:25269277
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Chen, H., Kilinski, L., and le Bihan, S.
TITLE AbcA5 transporter and uses thereof
JOURNAL Patent: WO 02070690-A 1 12-SEP-2002;
Active Pass Pharmaceuticals, Inc. (CA)
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AX417828
LOCUS AX417828 5262 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 5 from Patent WO0231147.
ACCESSION AX417828
VERSION AX417828.1 GI:21522944

KEYWORDS
SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
Hu, Y. and Nepomnichy, B.
AUTHORS
TITLE Human transporter proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0231147-A 5 18-APR-2002;
LEXICON GENETICS INC (US)

FEATURES

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ORIGIN

Query Match 80.4%; Score 5247.4; DB 6; Length 5262;
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VERSION AX417824.1 GI:21522942
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ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hu, Y. and Nepomnichy, B.
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LEXICON GENETICS INC (US)
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Qy	3471	CAGAGCTTACTTTTCTTGAAACCAAGGCTCTCTAGTGAGCACCATGAGCCTTTGG	3530
Db	2461	CAGAGCTTACTTTTCTTGAAACCAAGGCTCTCTAGTGAGCACCATGAGCCTTTGG	2520
Qy	3531	AAACCAACAGATGATACAAATAGCAAAATTTTCAATTTCTTTTACCTTGAAACGTGAAATGAA	3590
Db	2521	AAACCAACAGATGATACAAATAGCAAAATTTTCAATTTCTTTTACCTTGAAACGTGAAATGAA	2580
Qy	3591	TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT	3650
Db	2581	TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT	2640
Qy	3651	TTGGTTTCACTCTTTTAAATTTTCCCATCAAACTTTGTTCCAGACTTATAT	3710
Db	2641	TTGGTTTCACTCTTTTAAATTTTCCCATCAAACTTTGTTCCAGACTTATAT	2700
Qy	3711	TTTCTAAAACTGGAGACAAACACATAAATAACAAAAAAGTCTCTCTTCAAAATTTCT	3770
Db	2701	TTTCTAAAACTGGAGACAAACACATAAATAACAAAAAAGTCTCTCTTCAAAATTTCT	2760
Qy	3771	GCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAGCCAGAAACATATGTTGAGC	3830
Db	2761	GCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAGCCAGAAACATATGTTGAGC	2820
Qy	3831	ATGATTAATGACAGTGACTATGATATCCGTGGCTCCCATAGTGCAGCTTTAAATGTGTG	3890
Db	2821	ATGATTAATGACAGTGACTATGATATCCGTGGCTCCCATAGTGCAGCTTTAAATGTGTG	2880
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Qy	3951	CCATATATTAGTGAATATCATTAGTAACTACTATCTTTTCAATTTAAATGTGACTGAAACC	4010
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Qy	4011	ATCCAGATCTGGAGTACCCCATCTTTCAAGAAATTAAGTATATAGTTTTAAATGTGAG	4070
Db	3001	ATCCAGATCTGGAGTACCCCATCTTTCAAGAAATTAAGTATATAGTTTTAAATGTGAG	3060
Qy	4071	CTGTATTTTCAAGCAGCTTTGCTGGAATCATTTGTTTACTGCAATGCCACTTACTTTGCC	4130
Db	3061	CTGTATTTTCAAGCAGCTTTGCTGGAATCATTTGTTTACTGCAATGCCACTTACTTTGCC	3120
Qy	4131	ATGGAATAATCGAGAAATCATTAAGATCAAAAGCTTACTCAACTTTAAACCTTTCAAGTCTT	4190
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Qy	4191	TTGCCATCTGCATATTTGGATTTGGAACAGCTGTGTTGATATCCCTTATTTTATCAT	4250
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Qy	4251	CTTATTTTGGATGCTAGAGCTTACTGGAATTTCAATTTGATTTATTTTATCTGTA	4310
Db	3241	CTTATTTTGGATGCTAGAGCTTACTGGAATTTCAATTTGATTTATTTTATCTGTA	3300
Qy	4311	AAGTTCCTGCTGTGTTTTCCTTATTTGTTTATGTTTCCATCAGTATTTCTGTTCACT	4370
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Qy	4371	TATATTGCTCTCTTTCACCTTTAAAGAAATTTTAAATACCAAAGAAATTTTGGTCATTATTATC	4433
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Qy	4551	GGTTGCCCTGATTTCTTTTCATAAAGATTTCTTGGAGAAATCTAGCAAAAATATGGACACC	4610
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Qy	4611	TATAATCCATGGGATAGGCTTTTCAGTAGCTGTTTATATCGCTTATCGCTTACCTGCACTGTACTG	4670
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Qy	4671	TGGATTTTCTCTTTAATACTATGAGAAAAATATGGAGCGCAGATCAATAAGAAAGAT	4730
Db	3661	TGGATTTTCTCTTTAATACTATGAGAAAAATATGGAGCGCAGATCAATAAGAAAGAT	3720
Qy	4731	CCCTTTTTCAGAAACCTTTCAAACGAAGCTTAAATAAGGAAGCTTCCAGAAACCAACAGAC	4790
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Qy	5391	ACAGGTATGATCCCAAGCCAAACACAGATGTGGCGAGCAATTCGAACTGCATTTAAA	5450
Db	4381	ACAGGTATGATCCCAAGCCAAACACAGATGTGGCGAGCAATTCGAACTGCATTTAAA	4440
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VERSION				
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REFERENCE	1	Chen, H., Kilinski, L. and le Bihan, S.		
AUTHORS	Abca5 transporter and uses thereof			
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	/db_xref="taxon:9606"			
ORIGIN				
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Best Local Similarity	98.8%;	Pred. No. 0;		
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DB 3270 ATTATATTTTATPACTAAAGTCTCTGCTGTGTTTTTCCCTTATGTTATGTTCC 3329
QY 4352 ATCAGTTATCTGTTCACTATATTTGCTTCTTCACTTTTAAAGAAATTTTAAATACCAA 4411
DB 3330 ATCAGTTATCTGTTCACTATATTTGCTTCTTCACTTTTAAAGAAATTTTAAATACCAA 3389
QY 4412 AGAATTTTGTGCTATTTATCTTCTGTGAGCGGTTGCTGTTATTTGCAATCACTGAAAT 4471

DB 3390 AGAATTTTGTGCTATTTATCTATTTCTGTGGCAGGTTGGCTTGTATTTGCAATCACATGAAAT 3449
QY 4472 AACTTTCTTTATGGGATACAAATTCGAACTATTTCTTCAATATGCTTTTGTATCATAT 4531
DB 3450 AACTTTCTTTATGGGATACAAATTCGAACTATTTCTTCAATATGCTTTTGTATCATAT 3509
QY 4532 TCCAAATCTATCCACTTCTAGGTTGCTGATTTCTTCAATAAAGATTTCTTGAAGAATGT 4591
DB 3510 TCCAAATCTATCCACTTCTAGGTTGCTGATTTCTTCAATAAAGATTTCTTGAAGAATGT 3569
QY 4592 ACGAAAAAATGTGGACACCTTATTAATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCGCC 4651
DB 3570 ACGAAAAAATGTGGACACCTTATTAATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCGCC 3629
QY 4652 TTACTTGCAGTGTGTACTGTGGATTTTCTTCTACAAATACTATGAAAAAATATGAGG 4711
DB 3630 TTACTTGCAGTGTGTACTGTGGATTTTCTTCTTACAAATACTATGAAAAAATATGAGG 3689
QY 4712 CAGATCAATAAAGAAAAAGATCCCTTTTTCAGAAACCTTTTCAACGAAGCTTAAAAAATAGGAA 4771
DB 3690 CAGATCAATAAAGAAAAAGATCCCTTTTTCAGAAACCTTTTCAACGAAGCTTAAAAAATAGGAA 3749
QY 4772 GCTTCCAGAACCAACCCAGACAAATGAGGATGAAGATGAAGATGTCAAAAGCTGAAAGACTAA 4831
DB 3750 GCTTCCAGAACCAACCCAGACAAATGAGGATGAAGATGAAGATGTCAAAAGCTGAAAGACTAA 3809
QY 4832 GGTCAAGAGCTCATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTTATGCTCAGCAA 4891
DB 3810 GGTCAAGAGCTCATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTTATGCTCAGCAA 3869
QY 4892 TTTGCATAAAGAAATATGATGACAAAGAAATTTTCTTTCAGAAAGAAATGAAGAAAGT 4951
DB 3870 TTTGCATAAAGAAATATGATGACAAAGAAATTTTCTTCTTCAAGAAAGAAATGAAGAAAGT 3929
QY 4952 GGCATTAATATCATCTTCTTCTGCTGAAAAAGAGAGATCTTAGGACTATTTGGGCTCC 5011
DB 3930 GGCATTAATATCATCTTCTTCTGCTGAAAAAGAGAGATCTTAGGACTATTTGGGCTCC 3989
QY 5012 AATGTGTCTGGCAAAAGCACAATTAATATTTCTGTTGGTGATATTTGAACCAACTTC 5071
DB 3990 AATGTGTCTGGCAAAAGCACAATTAATATTTCTGTTGGTGATATTTGAACCAACTTC 4049
QY 5072 AGCCAGGTATTTTAGGAGATTTTCTTCAGAGACAAGTGAAGATGATGATTCATCTGAA 5131
DB 4050 AGCCAGGTATTTTAGGAGATTTTCTTCAGAGACAAGTGAAGATGATGATTCATCTGAA 4109
QY 5132 GTGTATGGGTTACTGTCTCAGATAAACCTTTTGTGGCCAGATPACTACATTCAGGAAACA 5191
DB 4110 GTGTATGGGTTACTGTCTCAGATAAACCTTTTGTGGCCAGATPACTACATTCAGGAAACA 4169
QY 5192 TTTTGAATTTTATGGAGCTGTCAAAGGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5251
DB 4170 TTTTGAATTTTATGGAGCTGTCAAAGGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4229
QY 5252 TCGAATAACACATGCTGCTGATTTTAAAGAAACATCTTCAAGAGCTGTAAGAAACTACC 5311
DB 4230 TCGAATAACACATGCTGCTGATTTTAAAGAAACATCTTCAAGAGCTGTAAGAAACTACC 4289
QY 5312 TGCAGGAATCAAAACGAAAGTGTGTTTTGCTCTAAGTATGCTAGGAAATCTCTCAGATTAC 5371
DB 4290 TGCAGGAATCAAAACGAAAGTGTGTTTTGCTCTAAGTATGCTAGGAAATCTCTCAGATTAC 4349
QY 5372 TTTTGTAGATGAACCATCTACAGTATGATCCCAAGCCAAACACACATGCTGGGAGC 5431
DB 4350 TTTTGTAGATGAACCATCTACAGTATGATCCCAAGCCAAACACACATGCTGGGAGC 4409
QY 5432 AATTCGAACCTGCAATTTAAAAACAGAAAGCGGGCTGCTATTTCTGACCCTCCTATATGGA 5491
DB 4410 AATTCGAACCTGCAATTTAAAAACAGAAAGCGGGCTGCTATTTCTGACCCTCCTATATGGA 4469
QY 5492 GGAGGAGAGGCTGTCTGTGATCGAGTACTATCATGTTGCTGCGGAGTTAAGATGAT 5551

Db	4470	GGAGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCGAGTTAAGATGTAT	4529
QY	5552	CGGAACAGTACACATCTAAGAGTAATTTGGABAGGCTACTTTTGGAAATTAAT	5611
Db	4530	CGGAACAGTACACATCTAAGAGTAATTTGGABAGGCTACTTTTGGAAATTAAT	4589
QY	5612	GAAGGAGCTGATAGAAAACCTAGAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTT	5671
Db	4590	GAAGGAGCTGATAGAAAACCTAGAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTT	4649
QY	5672	CCCAATGCAAGCGGTGAGAAAAGTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGA	5731
Db	4650	CCCAATGCAAGCGGTGAGAAAAGTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGA	4709
QY	5732	AGATGTTTCAGTCCCTTTCAAACTCTTTTAAAGCTGGAAGAGCTAAACATCTTTTGC	5791
Db	4710	AGATGTTTCAGTCCCTTTCAAACTCTTTTAAAGCTGGAAGAGCTAAACATCTTTTGC	4769
QY	5792	CATTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGCTTTTGTAGAACTCACTAA	5851
Db	4770	CATTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGCTTTTGTAGAACTCACTAA	4829
QY	5852	AGACRAGAGGAGGAAGATATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACG	5911
Db	4830	AGACRAGAGGAGGAAGATATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACG	4889
QY	5912	AACACAGAAGATAGAGTAGTATTTTGA	5939
Db	4990	AACACAGAAGATAGAGTAGTATTTTGA	4917
RESULT 10			
AX417826		4785 bp	DNA linear PAT 18-JUN-2002
LOCUS			
DEFINITION		Sequence 3 from Patent WO0231147.	
ACCESSION		AX417826	
VERSION		AX417826.1 GI:21522943	
KEYWORDS			
SOURCE			
ORGANISM		Homo sapiens (human)	
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
ORIGIN			
Query Match		72.9%; Score 4754.8; DB 6; Length 4785;	
Best Local Similarity		99.8%; Pred. No. 0;	
Matches 4756; Conservative		4; Mismatches 7; Indels 0; Gaps 0;	
QY	1011	ATGTCACATGCAATAGGAGGTAGGAGTTTGGAGACGACGACGACACATCTCTACTGAAG	1070
Db	1	ATGTCACATGCAATAGGAGGTAGGAGTTTGGAGACGACGACGACACATCTCTACTGAAG	60
QY	1071	AATTACTTAATTAATGAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA	1130
Db	61	AATTACTTAATTAATGAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA	120
QY	1131	TTTTTTTTTATTTTGGTTAATTAATAGCATGATGATCCAAATAGAAATATAGAGAA	1190
Db	121	TTTTTTTTTATTTTGGTTAATTAATAGCATGATGATCCAAATAGAAATATAGAGAA	180
QY	1191	GTGCTTAATATAGAACTCAATCTATGACAGTTTACTCTTCTAATCTAATCTTTGGA	1250
Db	181	GTGCTTAATATAGAACTCAATCTATGACAGTTTACTCTTCTAATCTAATCTTTGGA	240

QY	1251	TATATCTCAGTACATAATATTAAAGCAGCATCATGAGAAAGTGTCTCTGATCATCTA	1310
Db	241	TATATCTCAGTACATAATATTAAAGCAGCATCATGAGAAAGTGTCTCTGATCATCTA	300
QY	1311	CCTGATGTCATAATTTACTTGAAGATATACAAATGAAAGAAATGTTAAACATCAGTCTC	1370
Db	301	CCTGATGTCATAATTTACTTGAAGATATACAAATGAAAGAAATGTTAAACATCAGTCTC	360
QY	1371	TCTAAGCCGAGCAACTTTTGTAGTGTGGTTTCAAAGACTCCATGCTCTATGAATTCGT	1430
Db	361	TCTAAGCCGAGCAACTTTTGTAGTGTGGTTTCAAAGACTCCATGCTCTATGAATTCGT	420
QY	1431	TTTTTTCCTGATATGATTCAGATATCTTCTATTTATATGATTCAGAGCTGGCTGTTC	1490
Db	421	TTTTTTCCTGATATGATTCAGATATCTTCTATTTATATGATTCAGAGCTGGCTGTTC	480
QY	1491	AAATCATGTGAGGCTGCTCAGTACTGGTCTCAGCTTTTCAAGTTTCAAGCATCCATA	1550
Db	481	AAATCATGTGAGGCTGCTCAGTACTGGTCTCAGCTTTTCAAGTTTCAAGCATCCATA	540
QY	1551	GATGCTGCATTATACAGTTGAAACCAATGTTCTTTTGAAGAGCTGGAGTCAACT	1610
Db	541	GATGCTGCATTATACAGTTGAAACCAATGTTCTTTTGAAGAGCTGGAGTCAACT	600
QY	1611	AAAGCTGTTATATCGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA	1670
Db	601	AAAGCTGTTATATCGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA	660
QY	1671	ATTTTAAATATACCTAGTTTATAGCATTTTCACTTTTGGATACCTTTTGGCAATTCATATC	1730
Db	661	ATTTTAAATATACCTAGTTTATAGCATTTTCACTTTTGGATACCTTTTGGCAATTCATATC	720
QY	1731	GTAGCAGAAAAGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1790
Db	721	GTAGCAGAAAAGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	780
QY	1791	GCCTTTTGGCTTTCTCTGTTTCTCTATATACAACTTTTAAATTTTCTTATGTCCTTCT	1850
Db	781	GCCTTTTGGCTTTCTCTGTTTCTCTATATACAACTTTTAAATTTTCTTATGTCCTTCT	840
QY	1851	ATGCGAGTCATTGCGACAGCTCTTTTGTATTTTCTTCTTAAAGTAGCAGCATTTGTATTT	1910
Db	841	ATGCGAGTCATTGCGACAGCTCTTTTGTATTTTCTTCTTAAAGTAGCAGCATTTGTATTT	900
QY	1911	CTGCTTTTCTTCTTATGATTTATCATCTGTTATTTTCTTAAAGTAGCAGCATTTGTATTT	1970
Db	901	CTGCTTTTCTTCTTATGATTTATCATCTGTTATTTTCTTAAAGTAGCAGCATTTGTATTT	960
QY	1971	TTTTAAAAATCAAAACATGTGGAAATAGTTGTTTCTTCTTAAAGTAGCAGCATTTGTATTT	2030
Db	961	TTTTAAAAATCAAAACATGTGGAAATAGTTGTTTCTTCTTAAAGTAGCAGCATTTGTATTT	1020
QY	2031	ATGGCTTTATGATTAATCTCATAGAAAGTTTCCCAATCGTAGTGTGGCTTTTCACT	2090
Db	1021	ATGGCTTTATGATTAATCTCATAGAAAGTTTCCCAATCGTAGTGTGGCTTTTCACT	1080
QY	2091	CCCTTCTGCTGATCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	2150
Db	1081	CCCTTCTGCTGATCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	1140
QY	2151	AATGAAGGTGCTTCAATTTTCAAAATTTGACTGAGGCCCATATCTCTATTAATTAACAAT	2210
Db	1141	AATGAAGGTGCTTCAATTTTCAAAATTTGACTGAGGCCCATATCTCTATTAATTAACAAT	1200
QY	2211	ATCATGCTCACACTTAATAGTATATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	2270
Db	1201	ATCATGCTCACACTTAATAGTATATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1260
QY	2271	ATTCAGGGGAATTTGGCTTACGAGATCATCTTTATATTTTCTGAGGCTTCATATTGG	2330
Db	1261	ATTCAGGGGAATTTGGCTTACGAGATCATCTTTATATTTTCTGAGGCTTCATATTGG	1320

ACVAITETTFLOAYAVFVHYTFICIAIPIYVLLGCLISFIRKGSWKNMKNENTYNPW
DELLVAVIMPYLQCIWIFLQHYEKIHGGRSIRKDPFRFALSOXAKRKPPEPPINE
DEDEVDKARLKVLMGQCCCEKPAIMVNLHKEYDDKDFLHRSKXTTKVATKYIS
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ORIGIN

Query Match 59.6%; Score 3887; DB 10; Length 5347;

Best Local Similarity 85.0%; Pred. No. 0;

Matches 4381; Conservative 0; Mismatches 751; Indels 24; Gaps 2;

QY	991	AATAGGTTTATTCAGAAAAATGTCACCTGCAATTAGGAGGTAGGAGTTTGGACACAGA	1050
DB	190	AGTAACTGACCTAGAAAAATGGCTACTGCAATTAGGATGGGAGTTTGGACACAGA	249
QY	1051	CGAGAACCTTCTACTGAAGAATTACTTAATTAATGCGAACCAAAAAGAGTAGTGTC	1110
DB	250	CCAGAACCTTCTACTGAAAAATACCTAAATTAATGCGAGGACTAAAAAAGTAGTGTC	309
QY	1111	AGGAATTCCTTTTCCACTATTTTATTTTGGTTAATATTAATTAAGCATGATGCATC	1170
DB	310	AGGAATTCCTTTTCTCTATTTTCTATTTTGGCTGATATAGTTAGCATGATGCATC	369
QY	1171	CAAAATGAAGAAATATGAAGAGTGCCTATATATAGAACTCAATCCTATGGACAAAGTTTACTC	1230
DB	370	CAAAATGAAGAAATATGAAGAGTATCTGATATATAGAGTCCAGCCCTATGGACAAATTCAGCC	429
QY	1231	TTTCTAATCTAATCTTGTGATATCTCCAGTCAGCTAATATTAACAGAGCATCATGACAGA	1290
DB	430	TTTCCAGCTTATCTTGGATACATCTCCGCTGACTTAACATTAACAGAGCAATATGACAGA	489
QY	1291	AAGTGCTACTGATCATCTACCTGATGTGCATATTAATTAATTAAGAAATATCAAAATGAAGAAG	1350
DB	490	GGGTTTCTACCGATCATCTTCCAGGTTATAGTTACTGAAGAAATACGCAAAATGAGAAG	549
QY	1351	AAATGTTACATCCAGTCTCTTAAGCCGAGCAATCTTGTAGGTGGTGTTCAGAGACT	1410
DB	550	AACTGGTAGCCCAAGTCTTTCTAAGTCAGCAACTCTGAGGTGGTGTTCAGAGACA	609
QY	1411	CCATGTCCTATGAACCTTCGTTTTTCTCTGATGATCCAGTATCTTCTATTTATATGG	1470
DB	610	CCATGTCCTATGAACCTTCGTTTTTCTCTGAAATGATCCAGTGTCTTCTATTTATAGA	669
QY	1471	ATCAAGAGCTGGTGTTCAAAATCATGTGAGGCTGCTCAGTACGTGGTCTCAGGTTTCA	1530
DB	670	ATCAAGAGAGGCTGTTCAAAAGATGTGATGCTGCTCAGTACTGGTCTTTGGGGTTTA	729
QY	1531	CAGTTTTTCAAGCATCATPAGATGTGCCATATATACAGTTGAAGACCAATGTTTCTCTTT	1590
DB	730	CAGTTCTGAGGCATCGATAGATGTGCCATATATACAGCTGGAGACCAATGTTCTGTGT	789
QY	1591	GGAAGAGCTGGAGTCAACTAAGCTGTTTATATCGGAGAACTGCTCTGTGTAGAAATAG	1650
DB	790	GGAGCGAGCTGGAGTCGACCAAGCTGTGATCATGGGAGAGGCGCGCTGTGTGGAGATTG	849
QY	1651	ATACCTTTCCCGAGGAGTAATTTTAAATATACCTAGTTATAGCATTTTCACTTTTGGAT	1710
DB	850	ACACCTTTCCCGAGGAGGTCATCTCATCTCCTCGTCATAGCCCTTCTCGCCCTTCGGCT	909
QY	1711	ACTTTTGGCAATTCATATCGTAGCAAAAAAGAAAAAATAAAGAAATTTTAAAGA	1770
DB	910	ACTTCTGSCAATCCACATCGTGGCAGAAAAAGAAAGAGTAAAGGAAATTTTAAAGA	969
QY	1771	TAATGGAGCTTCATGATCTGCTTTTGGCTTTCTCTGGTTCCTCTATATACAGATTAA	1830
DB	970	TAATGGAGCTTCATGACACTGCTTTTGGCTTTCTCTGGTTCCTCTGTACGCAAGCTTGA	1029
QY	1831	TTTTTCTTATGTCCTTCTATGGCAGTCAITGGCAGAGCTTCTTTGTTATTTCTCTCAAA	1890

DB	1030	TTTTCTTATGTCCCTGCTTATGGCTGTCAATCCAAACAGCTTCTTGGTTATTTCCCTCAGA	1089
QY	1891	GTAGCAGCATGTGATATTTCTGCTTTTTTTCCTTTTATGGATTATCATCTGTATTTTTTG	1950
DB	1090	GTAGCAGCATGTGATCTTCTACTGCTCTCTTATATGAATGTGATCATCTGTGTTTTTG	1149
QY	1951	CTTTAATGCTGACACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTTTG	2010
DB	1150	CTTTAATGCTGACGCTCTTTTAAAAAATCAAAACACGTTGGGAGTCGTTGAGTTTTTTG	1209
QY	2011	TTACTGTGGCTTTTGGATTATTTGGCTTATGATAATCTCATAGAAAGTTTTCCTCAAT	2070
DB	1210	TCACCGTGGTGTGGATTGTGGCTGCTGATGCTCTCATAGAAAGTTTCCCAGGT	1269
QY	2071	CGTTAGTGGCTTTTCACTGCTTTTGTCACTGTAATCTTTTGTGATTTGTGATTTGCACAGG	2130
DB	1270	CGCTGGTGTGGCTCTTCACTGCTTTTGTGCTGCTGCTTTCTGATTTGGGATTTGCACAGG	1329
QY	2131	TCATGCATTTAGAGATTTTAAATGAAGGTGCTTCATTTTCAAAATTTGACTGCAGGCCAT	2190
DB	1330	TCATGCATTTAGAGATTTTAAATGAAGGTGCTTTATTTTCTAAATTTGACTGAAGTCCCT	1389
QY	2191	ATCCTCTAATTTATCAAAATTTATCATGCTCACACTTAATAGTATATTTCTATGCTCTTGG	2250
DB	1390	ATCCTCTAATTTATTAATTTATCATGCTTGTGACAGTGTGTTCTATGCTCTCTGG	1449
QY	2251	CTGCTCTATCTTGAATCAAGTCATTCAGGGGAATTTGGCTTACGGAGATCATCTTTATAT	2310
DB	1450	CTGCTATCTCGACCAAGTCATTCAGGGGAATTTGGCTTGAAGAGGTCACTCTTGTGAT	1509
QY	2311	TTCTGAAGCCTTCAVATTTGGTCAAGAGTAAAAAGAAATTTATGAGGAGTTATCAGAGGCA	2370
DB	1510	TTTTGAAGCCATGCTATTTGCTCAAAAACAAGAACTATTAAGAGCTATCGAGGCA	1569
QY	2371	ATGTTAATGAATAATAGTTTTAGTGAATTAATTGAGCCAGTTTCTTCAGAAATTTGTAG	2430
DB	1570	ACATTAATGCAATATAGTCTCAATGAATTTGTTGAGCCGTTTCTTCAGAAATTTATAG	1629
QY	2431	GAAGAAGCCATACGAATTTAGTGGTATTTCAGAGACATACAGAAAGAGGTGAAATG	2490
DB	1630	GGAAGAGCTATPAGAAATAGTGGTATTCAGAAATCTTATAGAAAGAAACTGGAAGC	1689
QY	2491	TGAGGCTTTGAGAAATTTGTCAATTTGACATATPAGAGGTGAGATTACTGCTTACTTG	2550
DB	1690	TGAGGCTTTGAGAAATTTGTCAATTTGACATATATGAAGGTGAGATTACTGCACTGCTG	1749
QY	2551	GCACAGTGGACAGAAAGAGTACATTTGATGAATTTCTTTGTGACCTCGCCACCTT	2610
DB	1750	GCACAGTGGACAGAAAGAGCACACTGATGAATTTCTGTGGACCGTGTCCACCT	1809
QY	2611	CTGATGGTTTGCATCTATATATGACACAGAGTCTCAGAAATAGATGAAATTTTGAAG	2670
DB	1810	CTGATGGTTTGTCTTATATATGACACAGAGTCTCTGAAATAGATGAAATATTTGAAG	1869
QY	2671	CAAGAAAAATGATGCGATTTGTCCACAGTTAGATATACCTTTGATGTTTTGACAGTAG	2730
DB	1870	CAAGAAAAATGATGCGCATATGTCCGAGTCAGATATAAACTTTGATGTTCTTGACAGTAG	1929
QY	2731	PAGAAAAATTTCAATTTTGGCTTCAATCAAAAGGATACAGCCAACTATAATACAG	2790
DB	1930	PAGAAAAATTTCAATTTTGGCTTCAATCAAGGAATACAGCCAACTATAATTAAG	1989
QY	2791	AAGTGCAAGGTTTTTACTAGATTTAGACATGACAGCTATCAAAAGATACCAAGCTAAAA	2850
DB	1990	AAGTGCAAGGTTTTTGTGCTGATCTGACATCGAAGCCATCAAGATATCAAGGAAAA	2049
QY	2851	AATTAAGTGGTGTCAAAAAGAAAGCTGCTCATTTAGGAATTCGTTCTTTGGGAAACCAA	2910
DB	2050	AGTTAAGCGGTGTGAGAAAGGAAGCTGTCTGTAGGAATTCAGTTCTCGGGAATCCAA	2109
QY	2911	AGATCTGCTGTGATGAACCAACAGCTGGAATGAGCCCTGTTCTCGACATATGTAT	2970
DB	2110	AGATACTCTCTGTAGACGAGCCTACAGCAGGAATGAGCCCTGCTCTCGCCCATTTGTTT	2169

QY	2971	GGAAATCTTTTAAATAACAGAAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGG	3030
Db	2170	GGBACTCTCTAAGTATAGAAAGCTAACAGAGTACCGGTGTTTAGTACTCACTTCATGG	2229
QY	3031	ATGAAGCTGACATCTTCTGGAGTAGAAAGCTGTGATATACAAAGGAATGCTGAAATGTG	3090
Db	2230	ATGAGGCTGACATCTTCCGCGACAGAAAGCTGTCATATCAAAAGGAATGCTGAAGTGTG	2289
QY	3091	TTGGTTCCTCAATGTTCCTCAAAAGTAATAGGGGATCGGCTACCGCTGAGCATGTACA	3150
Db	2290	TTGGTTCCTCAATGTTCCTCAAAAGTAATAGGGGATCGGCTACCGCTGAGCATGTATA	2349
QY	3151	TAGACAAATATTTGTGCCACAGAAATCTCTTTCTCACTGGTTAAACAACATATACCTGGAG	3210
Db	2350	TAGACAGATACTGTGCCACAGAGTCACTGTCTGCTGGTTAGGCAGACATACCCGCAG	2409
QY	3211	CTACTTATTAACAACAGATGACCAACACTTGTCTATAGTGTGCTTTCAAGGACATGG	3270
Db	2410	CCGCGTACTGACAGAGAATGACACAGAGTCTGTGTACAGCTGCCCTTCAAGACATGG	2469
QY	3271	ACAAATTTTCAGGTTTGTCTGCGCTAGACAGTCAATCAAAATTTGGGTGTCATTTCTT	3330
Db	2470	ACAAATTTTCAGGTTTGTCTGCGCTAGACATCAATCAAACTGGGTGTTATTTCTT	2529
QY	3331	ATGGTGTTCATGACGACTTTTGGAGAGTATTTTAAAGCTAGAGTTGAAGCAGAA	3390
Db	2530	ATGGTGTTCATGACGAAATTTGGAGAGTATTTTAAAGCTAGAGTTGAAGCAGAA	3389
QY	3391	TTGACCAAGCAGATTTATGTATTTTACTCAGCAGCCACTGGAGGAATAATGATTCAA	3450
Db	2590	TTGACCAAGCAGACTATGTATTTTACACAGCCGCGGAGGAGAAACAGATTCAA	2649
QY	3451	AATCTTTTATGAATGGAACAGAGCTTACTTATTTCTTCTGAAACCAAGCTTCTCTAG	3510
Db	2650	AATCTTTTATGAATGGAACAGAGTTTACTTATTTCTCTGAAACCAAGCTTCTCTAG	2709
QY	3511	TGAGCACCATGAGCCTTTGGAAACAACAGATGTATACAATAGCAAGTTTCATTTCTTTA	3570
Db	2710	TGAGCACCATGAGCCTTTGGAAACAACAGTGTCTACGATTTGCAAGTTTCATTTCTCT	2769
QY	3571	CCCTGAAACCTGAAAGTAATCATAGTGAATCATGTGTGCTTCTGCTTAAATTTTCTCA	3630
Db	2770	CATTGAACCCGAGAAACAAATCAGTGGCGCTGTGTGCTTCTGCTTAAATTTTCTTG	2829
QY	3631	CAGTTCAGATTTTATGTTTTTGGTTTCATCCTCTTTTAAATAATGCTGTGTTCCCATCA	3690
Db	2830	CAGTTCAGATTTTATGTTTTTCTCCATCATCTTTTAAATAATGCTGTGTTCCCATCA	2889
QY	3691	AACCTGTTCAGACTTATATTTTCTAAACCTGGAGACAAACCAATATAACAAACAA	3750
Db	2890	AACCTGTTCAGACTTATATTTTCTAAACCTGGAGATAAACCTCATATAACAAACAA	2949
QY	3751	GTCTGCTTCTCAAAATTTCTGCTGACTCAGATATCAGTATCTTATTAGCTTTTTCACAA	3810
Db	2950	GCCTGTGCTTCAAAATTTCTGCTGACTCAGATATCAATGGTCTTATTGAGTTTTTGAC	3009
QY	3811	GCCAGAACATAATGGTGACCATTAATGACAGTCACTATGTATCCGTGGCTCCCATATA	3870
Db	3010	ACCCAGAACATAATGGTGCAATGTTTAAATGACAGTCACTATGTGTCTGCTCTCTACA	3069
QY	3871	GTGCGGCTTAAATGTGATGCTATCAGAAAGACTATGTTTTTGCAGCTGTTTTTCACA	3930
Db	3070	GTGCGGCTTCAATGTGGTGGTCTTGAAGAGACTATGTTTTTCTGCTGTTTTTCAACA	3129
QY	3931	GTACTGTGGTTTATCTTTTACCTATATTAGTGAATCATTAATAGTAACACTATCTTTATC	3990
Db	3130	GTACTGTGGTTTATGTTTGCAGTCAATGATGAACATCATTAGTAACACTATCTTTATC	3189
QY	3991	ATTTAAATGTGACTGAAACCAATCCAGATCTGGAGTACCCCATCTTTTCAAGAAATTACTG	4050
Db	3190	ATTTAAATGTGACTGAAAGCCATCCAGACCTGGAGTACCCCGTTTCAATTAAGAAATTACTG	3249

QY	991	AATAGGTTTATTGAGAAAATGTCCTCACTGCAATTAGGGAGTAGGAGTTTGAGACAGA	1050	QY	2071	CGTTAGTGTGGCTTTTCAGTCTTCTGCTACTGTAATTTGTGATGATGATGACAGG	2130
Db	16	AGTAAGCTGACCTAGAAAACATGGCTACTGCAATTAGGGATGTGGCGTTTGAGACAGA	75	Db	1096	CGTATGTGGCTCTTCAGTCTTCTGCTGAGTGGCCCTTTCTGATTTGGGATTTGACACAGG	1155
QY	1051	CCAGAACACCTTCTACTGAAGAAATTAATTAATGACAGAACCAAAAAGAGTAGTGTTC	1110	QY	2131	TCATGCATTTAGAACATTTTAATGAAGTGTCTCAATTTTCAATTTGACTGACGCCCAT	2190
Db	76	CCAGAACACCTTCTCTGAGAAATTAACCTGCTCAATGCAGGACTAAAAGAGTAGTGTTC	135	Db	1156	TCATGCATTTAGAACATTTCAATGAAGAGGCTTAATTTTCTAGTTTGAAGGCCCT	1215
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JOURNAL Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp686K07118) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://mips.gsf.de/proj/cDNA/>.
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ORIGIN

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DB	1981	CAGTACTATGGTTTATCTTTTACTATATTAGTGTGAATATCATTTAGTAAACTACTATCTTTA	2040
QY	3989	TCAATTTAAATGTGACTTGAACCACTCCAGATCTCGAGTACCCCACTCTTTCAAGAAATTAC	4048
DB	2041	TCAATTTAAATGTGACTTGAACCACTCCAGATCTCGAGTACCCCACTCTTTCAAGAAATTAC	2100
QY	4049	TGATATAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTAC	4108
DB	2101	TGATATAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTAC	2160
QY	4109	TGCAATGCCACCTTACTTTGCCATGGAAATGCAGAGMATCATTAAGATCAAGCTTTATAC	4168
DB	2161	TGCAATGCCACCTTACTTTGCCATGGAAATGCAGAGMATCATTAAGATCAAGCTTTATAC	2220
QY	4169	TCAACTTAAACTTTTCCAGCTCTTTTGCCATCTGCATATTGGAATGGACAAGCTGTTGTGA	4228
DB	2221	TCAACTTAAACTTTTCCAGCTCTTTTGCCATCTGCATATTGGAATGGACAAGCTGTTGTGA	2280
QY	4229	TATCCCTTATTTTATATCAATCTTATTTTGTAGTGTAGGAAGCTTACTGGCAATTCATTA	4288
DB	2281	TATCCCTTATTTTATATCAATCTTATTTTGTAGTGTAGGAAGCTTACTGGCAATTCATTA	2340
QY	4289	TGATATATTTTATATCTGTAAGTTCCTTGTCTGTGTTTTTTTGCCTTATTTGGTTATGT	4348
DB	2341	TGATATATTTTATATCTGTAAGTTCCTTGTCTGTGTTTTTTTGCCTTATTTGGTTATGT	2400
QY	4349	TCCATCAGTTTATCTGTGTCACTTATATTTGCTTCTTTCAAGAAAAATTTTAAATAC	4408
DB	2401	TCCATCAGTTTATCTGTGTCACTTATATTTGCTTCTTTCAAGAAAAATTTTAAATAC	2460
QY	4409	CAAGAATTTTGGTCATTTATCTATTTCTGTGGCAGCGTTGNCCTTGATTTGCAATCACTGA	4468
DB	2461	CAAGAATTTTGGTCATTTATCTATTTCTGTGGCAGCGTTGNCCTTGATTTCAATCACTGA	2520

QY	4469	AAATACTTTCTTTATGGGATACACAATATGCAACTATTCTTCATTATAGCCTTTTGTATCAT	4526
DB	2521	AAATACTTTCTTTATGGGATACACAATATGCAACTATTCTTCATTATAGCCTTTTGTATCAT	2580
QY	4529	CAATCCAAATCTATCCACTTCTAGGTTGCTGTATTTCTTTCAATAAGATTTCTTTGGAAGAA	4588
DB	2581	CAATCCAAATCTATCCACTTCTAGGTTGCTGTATTTCTTTCAATAAGATTTCTTTGGAAGAA	2640
QY	4589	TGTCAGAAAAATATGGACACCTATAATCCATGGGATAGGCTTTTCACTAGCTGTTATATATC	4648
DB	2641	TGTCAGAAAAATATGGACACCTATAATCCATGGGATAGGCTTTTCACTAGCTGTTATATATC	2700
QY	4649	GCTTTACCTGCACTGTACTCTGTGATTTTCTCTTACAATACTATGAGAAAAATATGG	4708
DB	2701	GCTTTACCTGCACTGTACTCTGTGATTTTCTCTTACAATACTATGAGAAAAATATGG	2760
QY	4709	AGGCAGATCAATAAGAAAAAGATCCCTTTTTTCAGAAACCTTTCAACGAAGCTTAAAAATAG	4768
DB	2761	AGGCAGATCAATAAGAAAAAGATCCCTTTTTTCAGAAACCTTTCAACGAAGCTTAAAAATAG	2820
QY	4769	GAAGCTTCCAGAACCAACAGACAATGAGGATGAAGATGTCAAAGCTTCAAAAGACT	4828
DB	2821	GAAGCTTCCAGAACCAACAGACAATGAGGATGAAGATGTCAAAGCTTCAAAAGACT	2880
QY	4829	AAAGGTCAAAGAGCTGATGGGTTGCCAGTGTGTTGTGAGGAGAAACCATTCATTATGGTCAG	4888
DB	2881	AAAGGTCAAAGAGCTGATGGGTTGCCAGTGTGTTGTGAGGAGAAACCATTCATTATGGTCAG	2940
QY	4889	CAATTTGCAATAAGAAATATGATGACAGAAAGATTTTCTTCTTCAAGAAAGTAAAGAA	4948
DB	2941	CAATTTGCAATAAGAAATATGATGACAGAAAGATTTTCTTCTTCAAGAAAGTAAAGAA	3000
QY	4949	AGTGGCAACTAAATACATCTCTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGG	5008
DB	3001	AGTGGCAACTAAATACATCTCTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGG	3060
QY	5009	TCCAAATGCTGTGGCAAAAGCACAAATTAATAATCTTGGTTGGTGATATTGAACCAAC	5068
DB	3061	TCCAAATGCTGTGGCAAAAGCACAAATTAATAATCTTGGTTGGTGATATTGAACCAAC	3120
QY	5069	TTTCAGCCAGGTAATTTTATAGGAGATTTCTTCAGAGACAAGTGAAGATGATGATTCAT	5128
DB	3121	TTTCAGCCAGGTAATTTTATAGGAGATTTCTTCAGAGACAAGTGAAGATGATGATTCAT	3180
QY	5129	GAAGTGTATGGGTTACTGTCCTCAGATAAACCCCTTTGTGGCCAGATATCTACATTCAGGA	5188
DB	3181	GAAGTGTATGGGTTACTGTCCTCAGATAAACCCCTTTGTGGCCAGATATCTACATTCAGGA	3240
QY	5189	ACATTTTGAATTTATGGAGCTGTCAAGAGATGAGTCAAGTGACATGAAGAAGTCAAT	5248
DB	3241	ACATTTTGAATTTATGGAGCTGTCAAGAGATGAGTCAAGTGACATGAAGAAGTCAAT	3300
QY	5249	AAAGTCGAATAACACATGCACTTGATTTTAAAGAAACATCTTTCAGAAAGCTGTAAGAAGAACT	5308
DB	3301	AAAGTCGAATAACACATGCACTTGATTTTAAAGAAACATCTTTCAGAAAGCTGTAAGAAGAACT	3360
QY	5309	ACCTGCAGGAATCAAAACGAAAGTTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAGAT	5368
DB	3361	ACCTGCAGGAATCAAAACGAAAGTTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAGAT	3420
QY	5369	TACTTTTCTAGATGAACCATCTACAGATGAGATCCAAAGCCAAACAGACATGTTGGCG	5428
DB	3421	TACTTTTCTAGATGAACCATCTACAGATGAGATCCAAAGCCAAACAGACATGTTGGCG	3476
QY	5429	AGCAATTCGAATGCAATTTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCATTAT	5488
DB	3477	-----	3476
QY	5489	GGAGGAGCAGAGGCTGCTGTGTGATCGAGTAGCTATCATGGTGTCTGTGGCAGTTAAGATG	5548
DB	3477	-----GATG	3480
QY	5549	TATCGGAACAGTACAAACATCTAAAGAGTAATAATTGGAAAGGGCTACTTTTGTGAAATTA	5608

Mon Dec 6 10:08:08 2004

Db 3481 TATCGGAACAGTACAACTCTAAAGATAAATTTGGAAAGGCTACTTTTGGAAATTA 3540
Qy 5609 ATTGAAGGACTGGATAGAAAACCTTAGAAGTAGACCGCTTCAAAGAGAAATTCAGTATAT 5668
Db 3541 ATTGAAGGACTGGATAGAAAACCTTAGAAGTAGACCGCTTCAAAGAGAAATTCAGTATAT 3600
Qy 5669 TTTCCCAATGCAAGCCGTCAGGAAGTTTTCTTCTATTTTGGCTTATTAATTCCTAA 5728
Db 3601 TTTCCCAATGCAAGCCGTCAGGAAGTTTTCTTCTATTTTGGCTTATTAATTCCTAA 3660
Qy 5729 GGAAGATGTTTCAGTCCCTTTTCAACAATCTTTTTTAAGCTGGAAGAGCTAAACATGCTTT 5788
Db 3661 GGAAGATGTTTCAGTCCCTTTTCAACAATCTTTTTTAAGCTGGAAGAGCTAAACATGCTTT 3720
Qy 5789 TGCCATTGAAGATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCAC 5848
Db 3721 TGCCATTGAAGATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCAC 3780
Qy 5849 TAAAGAACAGAGGAGGAGATATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGA 5908
Db 3781 TAAAGAACAGAGGAGGAGATATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGA 3840
Qy 5909 ACGAACACAGAGATAGAGTAGTATTTTGAATTTGTATTTGTCGGTCTGCTTACTGGGA 5968
Db 3841 ACGAACACAGAGATAGAGTAGTATTTTGAATTTGTATTTGTCGGTCTGCTTACTGGGA 3900
Qy 5969 CTTCTTTCTTTTTCACCTTAATTTTAACTTTGGTTTAAAGTTTTTTTATTGGGAATGTAA 6028
Db 3901 CTTCTTTCTTTTTCACCTTAATTTTAACTTTGGTTTAAAGTTTTTTTATTGGGAATGTAA 3960
Qy 6029 CTGGAGAACCAAGAACGACCTTGAATTTTCTAAGCTCCTTAATTTGAAATGCTGTGTT 6088
Db 3961 CTGGAGAACCAAGAACGACCTTGAATTTTCTAAGCTCCTTAATTTGAAATGCTGTGTT 4020
Qy 6089 GTGTGTTTGTCTTTTCTTTAAATAAACGATATGATATTAAGTGAA 6135
Db 4021 GTGTGTTTGTCTTTTCTTTAAATAAACGATATGATATTAATTAATAAAAAA 4067

Search completed: December 4, 2004, 14:34:47
Job time : 26285 secs

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OM nucleic - nucleic search, using sw model
Run on: December 4, 2004, 04:56:06 ; Search time 2739 Seconds
(without alignments)
12505.466 Million cell updates/sec

Title: US-10-005-338B-1
Perfect score: 6525
Sequence: 1 aaatgttgcattttctct.....ttgatcataataagtgaat 6525

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4134886 seqs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseq1990s:*
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4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
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8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2003cs:*
11: Geneseq2003ds:*
12: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6524	100.0	6525	6	ABN89594 Human ATP
2	6524	100.0	6525	12	ADN06076 Antipsori
3	6122.8	93.8	6369	6	AAD33648 Human TRI
4	5708.8	87.5	6170	12	ADH22577 cDNA enco
5	5373.2	82.3	5475	10	ABSS5751 cDNA enco
6	5255.8	80.5	5463	10	ABSS57749 cDNA enco
7	5247.4	80.4	5262	6	AAD37620 Human tra
8	4918.4	75.4	4929	6	AAD37618 Human tra
9	4807.4	73.7	4917	10	ABSS57750 Coding se
10	4754.8	72.9	4785	6	AD37619 Human tra
11	3258.2	43.9	3347	11	ADM01475 Human cdn
12	3178	48.7	3268	10	ADA53416 Human cod
13	2934.4	45.0	3950	10	ADF74739 Murine dn
14	2807	43.0	3831	10	ADF74738 Murine dn
15	2683.8	41.1	2723	10	ADC51606 Human mac
16	2378.8	36.5	2481	8	AB235938 Human sec
17	1809.4	27.7	2325	10	ADF81819 Leukaemia
18	1789.4	27.4	3328	6	ABK35707 cDNA sequ
19	1731.8	26.5	1943	11	ADM02739 Human cdn
20	1722.8	26.4	1818	5	AA563176 Human pur
21	1543.8	23.7	1548	6	ABK35706 cDNA sequ

22	1319	20.2	1506	3	AAC81717 Human sec
23	1182	18.1	1346	6	ABL64459 Stomach c
24	1182	18.1	1346	6	ABL63763 Breast ca
25	1182	18.1	1346	6	ABN96909 Gene #340
26	1182	18.1	1346	10	ADH23065 Human chr
27	1150.4	17.6	6181	6	ABN89597 Human ATP
28	1149.8	17.6	5722	8	ABZ22923 Human ABC
29	1123.6	17.2	6112	12	ADM67036 Human hom
30	1122.4	17.2	5966	11	ADL33372 Human tra
31	1118.8	17.1	5981	6	ABN89596 Human ATP
32	1117.2	17.1	4875	8	ABSS57519 Human ABC
33	1117.2	17.1	5018	8	ABSS57518 Human ABC
34	1090.8	16.7	5296	6	ABN89595 Human ATP
35	1090.4	16.7	5797	9	ADA20300 Human ATP
36	1089.2	16.7	5211	8	AD47363 Human tra
37	1086	16.6	5332	6	ABQ77736 Human ABC
38	1084.6	16.6	5680	8	ABZ22922 Human ABC
39	1030.6	15.8	5125	12	ADJ27227 Human TRI
40	1020.2	15.1	6268	12	ADM67035 Human sec
41	982.2	15.6	1632	8	ABZ35926 Human tum
42	979	15.0	5311	10	ADD29639 Human TRI
43	933.2	14.3	5846	8	AAD49503 Human tra
44	930.6	14.3	4727	6	AAL44690 Human tra
45	930.6	14.3	5149	6	AAD33675 Human TRI

ALIGNMENTS

RESULT 1
ABN89594
ID ABN89594 standard; cDNA; 6525 BP.
XX
AC ABN89594;
XX
DT 18-SEP-2002 (first entry)
XX
DE Human ATP-binding cassette transporter ABCA5 cDNA SEQ ID NO:1.
XX
KW Human; ABCA5; ABCA6; ABCA9; ABCA10; ATP-binding cassette transporter;
KW chromosome 17; chromosome 17q; chromosome 17q24; antiarteriosclerotic;
KW gene therapy; cholesterol; lipophilic molecule; inflammation;
KW prostaglandin; prostacyclin; arteriosclerosis; transport; gene; ss.
XX
OS Homo sapiens.
XX
FN WC200246458-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-BP015401.
XX
PR 07-DEC-2000; 2000EP-00403440.
PR 23-JAN-2001; 2001US-0263231P.
PA (AVET) AVENTIS PHARMA SA.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Denefle P, Rosier-Montus M, Prades C, Arnould-Reguigne I;
PI Duverger N, Allikmets R, Dean M;
XX
DR WPI; 2002-557584/59.
DR P-PSDB; ABB81574.
XX
PT A novel nucleic acid corresponding to ATP-binding cassette transporter
PT genes and the encoded polypeptide, useful for preventing or treating a
PT dysfunction in reverse transport of cholesterol.
XX
PS Claim 1; Page 151-153; 216pp; English.
XX
CC The present invention describes human ATP-binding cassette transporters
CC (ABC). Specifically described are the human ABCA5, ABCA6, ABCA9 and
CC ABCA10 genes (see ABN89594 to ABN89597) which encode the proteins given

QY	1861	TTGCGACAGCTTCCTTTGTTATATTTTCCTCAAGTAGCAGCATTTGTGATATTTCTGCTTTTTT	1920	2941	GAATGGACCCCTGTTCTCGACATATTTGTATGGAATCTTTTAAAAATACAGAAAAAGCCAAATC	3000	
Db	1861	TTGCGACAGCTTCCTTTGTTATATTTTCCTCAAGTAGCAGCATTTGTGATATTTCTGCTTTTTT	1920	QY	3001	GGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTCACATAGGAAG	3060
QY	1921	TCCTTTATGATATCATCTGATTTTTCCTTTTAAATGCTGACACCTCTTTTAAAAAAT	1980	Db	3001	GGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTCACATAGGAAG	3060
Db	1921	TCCTTTATGATATCATCTGATTTTTCCTTTTAAATGCTGACACCTCTTTTAAAAAAT	1980	QY	3061	CTGTGATATCAAGGAATGCTGAAATGTGTGTGTTCTTCAATGTCTCTCAAAAGTAAAT	3120
QY	1981	CAAAAANGTGGGAATAGTTGAAATTTTGTGTTACTGTGGCTTTTGGATTTATGGCCCTTA	2040	Db	3061	CTGTGATATCAAGGAATGCTGAAATGTGTGTGTTCTTCAATGTCTCTCAAAAGTAAAT	3120
Db	1981	CAAAAANGTGGGAATAGTTGAAATTTTGTGTTACTGTGGCTTTTGGATTTATGGCCCTTA	2040	QY	3121	GGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTTGGCCACAAATCTCTTT	3180
QY	2041	TGATAATCCCTATAGAAAAGTTTCCCAAATCGTTAGTGGCTTTTCAAGTCTCTCTGTC	2100	Db	3121	GGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTTGGCCACAAATCTCTTT	3180
Db	2041	TGATAATCCCTATAGAAAAGTTTCCCAAATCGTTAGTGGCTTTTCAAGTCTCTCTGTC	2100	QY	3181	CTTCACTGGTTAAACAAATATACCTGGAGCTACTTTATTACACAGAAATGACCAACAAC	3240
QY	2101	ACTGTACTTTTGTGATTTGATTTGACAGGTCATGCAATTTAGAGATTTTAAATGAAGGTG	2160	Db	3181	CTTCACTGGTTAAACAAATATACCTGGAGCTACTTTATTACACAGAAATGACCAACAAC	3240
Db	2101	ACTGTACTTTTGTGATTTGATTTGACAGGTCATGCAATTTAGAGATTTTAAATGAAGGTG	2160	QY	3241	TTGTGTATAGCTTGGCTTTCAAGGACATGGAACAAATTTTCAGGTTTGTCTGCCCCTAG	3300
QY	2161	CTTCAATTTCAAAATTCAGCTGAGGCCATATCTCTAAATTTATACAAATTTATCATGCTCA	2220	Db	3241	TTGTGTATAGCTTGGCTTTCAAGGACATGGAACAAATTTTCAGGTTTGTCTGCCCCTAG	3300
Db	2161	CTTCAATTTCAAAATTCAGCTGAGGCCATATCTCTAAATTTATACAAATTTATCATGCTCA	2220	QY	3301	ACAGTCATTTCAAAATTTGGGTGTCATTTCTTATGGTGTTCATGACGACTTTTGGAAAGCG	3360
QY	2221	CACTTAATAGTATTTCTATGTCCTCTTGGCTGTCTATCTTGATCAAGTCATTTCCAGGGG	2280	Db	3301	ACAGTCATTTCAAAATTTGGGTGTCATTTCTTATGGTGTTCATGACGACTTTTGGAAAGCG	3360
Db	2221	CACTTAATAGTATTTCTATGTCCTCTTGGCTGTCTATCTTGATCAAGTCATTTCCAGGGG	2280	QY	3361	TATTTTAAAGCTAGAAGTTGAAGCAGAAATTTGACCAAGCAGATTTATAGTGTATTTACTC	3420
QY	2281	AATTTGGCTTACGAGATCATCTTTATATTTCTGAAGCCTTCATATTTGGTCAAGAGTA	2340	Db	3361	TATTTTAAAGCTAGAAGTTGAAGCAGAAATTTGACCAAGCAGATTTATAGTGTATTTACTC	3420
Db	2281	AATTTGGCTTACGAGATCATCTTTATATTTCTGAAGCCTTCATATTTGGTCAAGAGTA	2340	QY	3421	ACAGCCACTGAGGAGAAATGGAATCAAAATCTTTTGTGAAATGGAACAGAGCTTAC	3480
QY	2341	AAAGAAATTTAGGAGTTATCAGAGGCAATGTTAATGGAATATTTAGTTAGTGAAA	2400	Db	3421	ACAGCCACTGAGGAGAAATGGAATCAAAATCTTTTGTGAAATGGAACAGAGCTTAC	3480
Db	2341	AAAGAAATTTAGGAGTTATCAGAGGCAATGTTAATGGAATATTTAGTTAGTGAAA	2400	QY	3481	TTATTTCTTCTGAAACCAAGGCTTCTTAGTGAGCACCATGAGCTTTGGAAACAAACAGA	3540
QY	2401	TTATTTAGCCAGTTTCTTCAAGATTTGTAGAAAGAGCCATTAAGAAATTTAGTGGTATC	2460	Db	3481	TTATTTCTTCTGAAACCAAGGCTTCTTAGTGAGCACCATGAGCTTTGGAAACAAACAGA	3540
Db	2401	TTATTTAGCCAGTTTCTTCAAGATTTGTAGAAAGAGCCATTAAGAAATTTAGTGGTATC	2460	QY	3541	TGTATACAAATAGCAAAAGTTTCAATTTCTTTTACCTTGAACCTGAAAGTAAATCAGTGAGAT	3600
QY	2461	AGAGACATACAGAAAGAGGTCGAAATTTGGAGGCTTTGAGAAATTTGTCAATTTGACAC	2520	Db	3541	TGTATACAAATAGCAAAAGTTTCAATTTCTTTTACCTTGAACCTGAAAGTAAATCAGTGAGAT	3600
Db	2461	AGAGACATACAGAAAGAGGTCGAAATTTGGAGGCTTTGAGAAATTTGTCAATTTGACAC	2520	QY	3601	CAGTGTGCTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTTTTGGTTTTCATC	3660
QY	2521	TATATGAGGGTCAGATTTACTGCCCTTACTTTGCCACAGTGGAAACAGGAAAGTACATGA	2580	Db	3601	CAGTGTGCTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTTTTGGTTTTCATC	3660
Db	2521	TATATGAGGGTCAGATTTACTGCCCTTACTTTGCCACAGTGGAAACAGGAAAGTACATGA	2580	QY	3661	ACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTTGTTCCAGCTTATATTTTCTAAAAAC	3720
QY	2581	TGAATATTTCTTTGGAGCTCTGCCACCTTCTGTATGGTTTGGATCTATATATGACACA	2640	Db	3661	ACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTTGTTCCAGCTTATATTTTCTAAAAAC	3720
Db	2581	TGAATATTTCTTTGGAGCTCTGCCACCTTCTGTATGGTTTGGATCTATATATGACACA	2640	QY	3721	CTGGAGACAAACACATATAATACAAACAGTCTGCTTCTTCAAAATTTCTGCTGACTCAG	3780
QY	2641	GAGTCTCAGAAATAGATGAATTTTGAAGCAAGAAATGATTTGGCATTTTGTCCACAGT	2700	Db	3721	CTGGAGACAAACACATATAATACAAACAGTCTGCTTCTTCAAAATTTCTGCTGACTCAG	3780
Db	2641	GAGTCTCAGAAATAGATGAATTTTGAAGCAAGAAATGATTTGGCATTTTGTCCACAGT	2700	QY	3781	ATATCAGTGATCTTATTTAGCTTTTTCACAAAGCAGAAACATAATGTTGACGATTAATG	3840
QY	2701	TAGATATACATTTGATTTTGAAGTAGAAGAAATTTATCAATTTTGGCTTCAATCA	2760	Db	3781	ATATCAGTGATCTTATTTAGCTTTTTCACAAAGCAGAAACATAATGTTGACGATTAATG	3840
Db	2701	TAGATATACATTTGATTTTGAAGTAGAAGAAATTTATCAATTTTGGCTTCAATCA	2760	QY	3841	ACAGTGATATGATCGGTGCTCCCATAGTGGGCTTTAAATGTTGATGATTCAGAAA	3900
QY	2761	AAGGATACCCGCAACATATAATACAAAGTGCAGAGGTTTACTAGATTTAGACA	2820	Db	3841	ACAGTGATATGATCGGTGCTCCCATAGTGGGCTTTAAATGTTGATGATTCAGAAA	3900
Db	2761	AAGGATACCCGCAACATATAATACAAAGTGCAGAGGTTTACTAGATTTAGACA	2820	QY	3901	AGGACTATGTTTTGAGCTGTTTTTCAACAGTACTATGTTTTTATTTTACCTTATATTAG	3960
QY	2821	TGCAGACTATCAAGATTAACCAAGCTTAAATAATTAAGTGGTGGTCAAAAAGAAAGCTGT	2880	Db	3901	AGGACTATGTTTTGAGCTGTTTTTCAACAGTACTATGTTTTTATTTTACCTTATATTAG	3960
Db	2821	TGCAGACTATCAAGATTAACCAAGCTTAAATAATTAAGTGGTGGTCAAAAAGAAAGCTGT	2880	QY	3961	TGAATATCATTTAGTAACTACTATCTTTTCAATTTAAATGTTGATGAACCATCCAGATCT	4020
QY	2881	CATTAGGAATTCCTGTTCTTTGGGAACCAAGATCTGCTAGATGAACCAAGCTGT	2940	Db	3961	TGAATATCATTTAGTAACTACTATCTTTTCAATTTAAATGTTGATGAACCATCCAGATCT	4020
Db	2881	CATTAGGAATTCCTGTTCTTTGGGAACCAAGATCTGCTAGATGAACCAAGCTGT	2940	QY	4021	GGAGTACCCCATCTTTTCAAGAAATTTACTGATATAGTTTTTAAAAATTTGACTGTATTTTC	4080
QY	2941	GAATGGACCCCTGTTCTCGACATATTTGTATGGAATCTTTTAAAAATACAGAAAAAGCCAAATC	3000				

Db	1141	TTTTGGTTAATATTAATAGCATGATGCATCCAAATAAGAAATATGAAGAAGTGCTAATA	1200	Db	2221	CACCTTAATAGTATPATTCTATGTCTCTTGCTGTCTATCTTGATCAAGTCATTCCAGGGG	2280
Qy	1201	TAGAAGTCAATCCTATGGCAAGTTTACTCTTTCTAATCTAATCTTGGATATATCTCCAG	1260	Qy	2281	AAATTTGGCTTACGGAGATCATCTTTATATATTTCTGAAGCCTTTCAATTTGGTCAAGAGATG	2340
Db	1201	TAGAACTCAATCCTATGGCAAGTTTACTCTTTCTAATCTAATCTTGGATATATCTCCAG	1260	Db	2281	AAATTTGGCTTACGGAGATCATCTTTATATATTTCTGAAGCCTTTCAATTTGGTCAAGAGATG	2340
Qy	1261	TGAACTAATATTACAAGCAGCATCATGCGAAGAGTGTCTACTGATCATCTACTGATGTCA	1320	Qy	2341	AAAGAAATATGAGGAGTTTATCAGAGGGCAATGTTAATGGAAATATTTAGTTTGTAGTAAA	2400
Db	1261	TGAACTAATATTACAAGCAGCATCATGCGAAGAGTGTCTACTGATCATCTACTGATGTCA	1320	Db	2341	AAAGAAATATGAGGAGTTTATCAGAGGGCAATGTTAATGGAAATATTTAGTTTGTAGTAAA	2400
Qy	1321	TAATTAAGAAATATACAAGTAAAGAAAGAAATGTTAAACATCCAGTCTCTTAAGCCGA	1380	Qy	2401	TTAATTCAGCCAGTTCTTCTCAGAAATTTGTAGGAAAAGAACCCATAGAATTTAGTGGTATTC	2460
Db	1321	TAATTAAGAAATATACAAGTAAAGAAAGAAATGTTAAACATCCAGTCTCTTAAGCCGA	1380	Db	2401	TTAATTCAGCCAGTTCTTCTCAGAAATTTGTAGGAAAAGAACCCATAGAATTTAGTGGTATTC	2460
Qy	1381	GAACTTTCTAGGTGTTGTTTTCAAGACTCCATGTCCTATGAACCTTCGTTTTTTTCTG	1440	Qy	2461	AGAAGACATACAGAAAGAGGGTGAATAATGTGGAGCTTTGAGAAATTTGTCAATTGACA	2520
Db	1381	GAACTTTCTAGGTGTTGTTTTCAAGACTCCATGTCCTATGAACCTTCGTTTTTTTCTG	1440	Db	2461	AGAAGACATACAGAAAGAGGGTGAATAATGTGGAGCTTTGAGAAATTTGTCAATTGACA	2520
Qy	1441	ATATGATTCAGTATCTTCTATTTATATGATTCAGAGCTGGCTGTTCAAAATCATGTG	1500	Qy	2521	TATATGAGGGTCAGATTACTGCTTACTTTGGCCACACAGTCGAAACAGAGAGAGTACATTGA	2580
Db	1441	ATATGATTCAGTATCTTCTATTTATATGATTCAGAGCTGGCTGTTCAAAATCATGTG	1500	Db	2521	TATATGAGGGTCAGATTACTGCTTACTTTGGCCACACAGTCGAAACAGAGAGAGTACATTGA	2580
Qy	1501	AGGCTGCTCAGTACTGGTCTCAGGTTTCAAGACTCCATGTCCTATGAACCTTCGTTTTTTTCTG	1560	Qy	2581	TGAATATTTCTTTGTGACTCTGCCACCTTTCTGATGGGTTTGCATCTATATATGGACACA	2640
Db	1501	AGGCTGCTCAGTACTGGTCTCAGGTTTCAAGACTCCATGTCCTATGAACCTTCGTTTTTTTCTG	1560	Db	2581	TGAATATTTCTTTGTGACTCTGCCACCTTTCTGATGGGTTTGCATCTATATATGGACACA	2640
Qy	1561	TTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACTAAGCTGTTA	1620	Qy	2641	GAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAATATGATGGCATTTCCTCACAGT	2700
Db	1561	TTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACTAAGCTGTTA	1620	Db	2641	GAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAATATGATGGCATTTCCTCACAGT	2700
Qy	1621	TTATGGGAAACTGCTGTTGTAGAAAATAGATACCTTTCCCGAGGAGTAATTTAATAT	1680	Qy	2701	TAGATATACACTTTGATGTTTTCAGACAGTAAAGAAATTTATCAATTTTGGCTTCAATCA	2760
Db	1621	TTATGGGAAACTGCTGTTGTAGAAAATAGATACCTTTCCCGAGGAGTAATTTAATAT	1680	Db	2701	TAGATATACACTTTGATGTTTTCAGACAGTAAAGAAATTTATCAATTTTGGCTTCAATCA	2760
Qy	1681	ACCTAGTTATAGCATTTTCACTTTTGGATACCTTTTGGCAATTCATATCGTAGCAGAAA	1740	Qy	2761	AAGGGATACAGCAACAATAATAACAAGAGTGCAGAAAGGTTTACTAGATTTTAGACA	2820
Db	1681	ACCTAGTTATAGCATTTTCACTTTTGGATACCTTTTGGCAATTCATATCGTAGCAGAAA	1740	Db	2761	AAGGGATACAGCAACAATAATAACAAGAGTGCAGAAAGGTTTACTAGATTTTAGACA	2820
Qy	1741	AGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACGCTTTTGGC	1800	Qy	2821	TGCAGACTCAAGATAACCAAGCTTAAATAATTAAGTGTGTCAAAAAAGAAAGCTGT	2880
Db	1741	AGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACGCTTTTGGC	1800	Db	2821	TGCAGACTCAAGATAACCAAGCTTAAATAATTAAGTGTGTCAAAAAAGAAAGCTGT	2880
Qy	1801	TTTCTGGGTTCTCTATATACAGTTTAAATTTTCTTATGTCCTTCTTATGGCAGTCA	1860	Qy	2881	CATTAGGAATGCTGTTCTTGGGAACCCAAAGATCTGCTGTAGATGAACCAAGCTGT	2940
Db	1801	TTTCTGGGTTCTCTATATACAGTTTAAATTTTCTTATGTCCTTCTTATGGCAGTCA	1860	Db	2881	CATTAGGAATGCTGTTCTTGGGAACCCAAAGATCTGCTGTAGATGAACCAAGCTGT	2940
Qy	1861	TTGCGACAGCTTCTTTGTTATTTCTCAAGTAGCAGCATTTGTGATATTTCTGTTTTTT	1920	Qy	2941	GAATGGACCCCTGTTCTCGACATATTTGATGGAATCTTTTAAATAACAGAAAGCCAATC	3000
Db	1861	TTGCGACAGCTTCTTTGTTATTTCTCAAGTAGCAGCATTTGTGATATTTCTGTTTTTT	1920	Db	2941	GAATGGACCCCTGTTCTCGACATATTTGATGGAATCTTTTAAATAACAGAAAGCCAATC	3000
Qy	1921	TGCTTTATGATATCATCTGATTTTGTGCTTAACTGCTGACCTCTTTTAAATAAT	1980	Qy	3001	GGGTGACAGTGTTCAGTACTCATTTTCATGATGAAGCTGACATTTCTTGAGATAGAAAG	3060
Db	1921	TGCTTTATGATATCATCTGATTTTGTGCTTAACTGCTGACCTCTTTTAAATAAT	1980	Db	3001	GGGTGACAGTGTTCAGTACTCATTTTCATGATGAAGCTGACATTTCTTGAGATAGAAAG	3060
Qy	1981	CAAAACATGTGGGAATGATTTTGTGTTACTGTGGCTTTTGGATTTATGCGCTTA	2040	Qy	3061	CTGTGATATCAAGGAATGCTGAAATGTTGGTTCCTCAATGTTCTTCAAAAGTAAT	3120
Db	1981	CAAAACATGTGGGAATGATTTTGTGTTACTGTGGCTTTTGGATTTATGCGCTTA	2040	Db	3061	CTGTGATATCAAGGAATGCTGAAATGTTGGTTCCTCAATGTTCTTCAAAAGTAAT	3120
Qy	2041	TGATAATCCTCATAGAAATTTTCCAAATCGTTAGTGGCTTTTCAAGTCTTCTGTC	2100	Qy	3121	GGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTTGTGCCACAGAAATCTCTTT	3180
Db	2041	TGATAATCCTCATAGAAATTTTCCAAATCGTTAGTGGCTTTTCAAGTCTTCTGTC	2100	Db	3121	GGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTTGTGCCACAGAAATCTCTTT	3180
Qy	2101	ACTGTACTTTTGTGATTTGATTTGACAGGTCATGCAATTTAGAATTTTAAATGAAGTG	2160	Qy	3181	CTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATTAACAAGATGACCAACAC	3240
Db	2101	ACTGTACTTTTGTGATTTGATTTGACAGGTCATGCAATTTAGAATTTTAAATGAAGTG	2160	Db	3181	CTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATTAACAAGATGACCAACAC	3240
Qy	2161	CTTCAATTTCAATTTGATCGAGGCCCATATCCTCTAATTTAATTAATATCATGCTCA	2220	Qy	3241	TTCTGTATAGCTTGCCTTCAAGGACATGACAAATTTTCAAGTGTGTTTCTGCCCTAG	3300
Db	2161	CTTCAATTTCAATTTGATCGAGGCCCATATCCTCTAATTTAATTAATATCATGCTCA	2220	Db	3241	TTCTGTATAGCTTGCCTTCAAGGACATGACAAATTTTCAAGTGTGTTTCTGCCCTAG	3300
Qy	2221	CACCTAATAGTATATCTATGCTTCTGCTGCTATCTTGTATGATCAAGTCAATCCAGGGG	2280	Qy	3301	ACAGTCAATTTGGGTGTCATTTCTTATGGTGTGTTTCCATGACGACTTTTGGAGAGG	3360
Db	2221	CACCTAATAGTATATCTATGCTTCTGCTGCTATCTTGTATGATCAAGTCAATCCAGGGG	2280	Db	3301	ACAGTCAATTTGGGTGTCATTTCTTATGGTGTGTTTCCATGACGACTTTTGGAGAGG	3360

QY	3361	TATTTTAAAGCTAGAGTTGAAGCAGAAAATTGACCAAGCAGATATATAGTGTATTTACTC	3420	4441	CAGCGTGNCTTGTAATTGGCAATCACTGAAATAATCTTTCTTTATGGGATACACAATTCGAA	4500
DB	3361	TATTTTAAAGCTAGAGTTGNAAGCAGAAAATTGACCAAGCAGATATATAGTGTATTTACTC	3420	4441	CAGCGTGNCTTGTAATTGGCAATCACTGAAATAATCTTTCTTTATGGGATACACAATTCGAA	4500
QY	3421	AGCAGCCACTGAGGAGAAATGGAAATCAAAATCTTTTGTATGAAATGGAAACAGAGCTTAC	3480	4501	CTATTTCTTCATTAATGCGCTTTTGTATCATCATTCCAATCTATCCACTTTAGGTTCGCTGA	4560
DB	3421	AGCAGCCACTGAGGAGAAATGGAAATCAAAATCTTTTGTATGAAATGGAAACAGAGCTTAC	3480	4501	CTATTTCTTCATTAATGCGCTTTTGTATCATCATTCCAATCTATCCACTTTAGGTTCGCTGA	4560
QY	3481	TTATTTCTTTCTGAAACCAAGGCTCTCTAGTGTAGCACCATGAGCTTTTGGAAACACAGAG	3540	4561	TTTCTTTCTATAAAGATTTCTTGGAGAAATGTACGAAAAAATGTGGACACCTATAATTCAT	4620
DB	3481	TTATTTCTTTCTGAAACCAAGGCTCTCTAGTGTAGCACCATGAGCTTTTGGAAACACAGAG	3540	4561	TTTCTTTCTATAAAGATTTCTTGGAGAAATGTACGAAAAAATGTGGACACCTATAATTCAT	4620
QY	3541	TGTATACAAATAGCAAAAGTTTCAATTTCTTTACCTTTGAAACGTTGAAAGTAATTCAGTGAGAT	3600	4621	GGGATAGGCTTTTCAAGTGTATATATCGCTTACCTGCAGTGTGTACTGTGCAATTTTCC	4680
DB	3541	TGTATACAAATAGCAAAAGTTTCAATTTCTTTACCTTTGAAACGTTGAAAGTAATTCAGTGAGAT	3600	4621	GGGATAGGCTTTTCAAGTGTATATATCGCTTACCTGCAGTGTGTACTGTGCAATTTTCC	4680
QY	3601	CAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTTGTGTTTCAAC	3660	4681	TCTTTACAAATACTATGAGAAAAAATATGGAGGCAGATCAATAAGAAAAAGATCCCTTTTCA	4740
DB	3601	CAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTTGTGTTTCAAC	3660	4681	TCTTTACAAATACTATGAGAAAAAATATGGAGGCAGATCAATAAGAAAAAGATCCCTTTTCA	4740
QY	3661	ACTCTTTTAAAAATGCTGTGTTCCCATCAAACTTGTTCCAGACTTATTTCTAAAAAC	3720	4741	GAAACCTTTCAACCAAGCTCTAAAAATAGGAAGCTTCCAGAACACACAGACAATGAGGATG	4800
DB	3661	ACTCTTTTAAAAATGCTGTGTTCCCATCAAACTTGTTCCAGACTTATTTCTAAAAAC	3720	4741	GAAACCTTTCAACCAAGCTCTAAAAATAGGAAGCTTCCAGAACACACAGACAATGAGGATG	4800
QY	3721	CTGGAGACAAAACACATAAATACAAAACAGTCTGCTTTCTTCAAAATTTCTGCTGACTCAG	3780	4801	AAGATGAAGATGTCABAGCTGAAAGACTAAAGGTCAAGAGCTGATGGGTTCGCACTGTT	4860
DB	3721	CTGGAGACAAAACACATAAATACAAAACAGTCTGCTTTCTTCAAAATTTCTGCTGACTCAG	3780	4801	AAGATGAAGATGTCABAGCTGAAAGACTAAAGGTCAAGAGCTGATGGGTTCGCACTGTT	4860
QY	3781	ATATCAGTGATCTTATAGCTTTTTCACAAGCCAGAACATAATGGTCACGATGATTAAATG	3840	4861	GTGAGGAGAAAACCATTCATTTATGGTCAGCAATTTGTCAATAAGNATATGATGACAGAAAG	4920
DB	3781	ATATCAGTGATCTTATAGCTTTTTCACAAGCCAGAACATAATGGTCACGATGATTAAATG	3840	4861	GTGAGGAGAAAACCATTCATTTATGGTCAGCAATTTGTCAATAAGNATATGATGACAGAAAG	4920
QY	3841	ACAGTACATGATGATCCGTTGGCTCCCATPAGTGGCGCTTTAAATGTGATGCAATTCAGAAA	3900	4921	ATTTTCTCTTTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATAACATCTCTTTCTGTGCA	4980
DB	3841	ACAGTACATGATGATCCGTTGGCTCCCATPAGTGGCGCTTTAAATGTGATGCAATTCAGAAA	3900	4921	ATTTTCTCTTTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATAACATCTCTTTCTGTGCA	4980
QY	3901	AGCAGTATGTTTTTGCAGCTGTTTTCAACAGTACTATGTTTATTTCTTTACTATATAG	3960	4981	AAAAAGAGAGATCTTAGGACTATTTGGTGTCAAATGGTGTCTGCAAAAGCACAATTTATTA	5040
DB	3901	AGCAGTATGTTTTTGCAGCTGTTTTCAACAGTACTATGTTTATTTCTTTACTATATAG	3960	4981	AAAAAGAGAGATCTTAGGACTATTTGGTGTCAAATGGTGTCTGCAAAAGCACAATTTATTA	5040
QY	3961	TGAATATCATAGTAACACTATCTTTATCATTTTAAATGTGACTGAAACCATCCAGATCT	4020	5041	ATATTTCTGGTTGGTGATTTGAAACCACTTTGAGCCAGGTATTTTTAGGAGATTTATCTTT	5100
DB	3961	TGAATATCATAGTAACACTATCTTTATCATTTTAAATGTGACTGAAACCATCCAGATCT	4020	5041	ATATTTCTGGTTGGTGATTTGAAACCACTTTGAGCCAGGTATTTTTAGGAGATTTATCTTT	5100
QY	4021	GGAGTACCCCATTTCTTCAAGAAATTTACTGATATAGTTTTTAAATTTGAGCTGTATTTTC	4080	5101	CAGAGACAAGTCAAGATGATTTCACTGAAGTGTATGGGTATCTGTCTCTCAGATTAACC	5160
DB	4021	GGAGTACCCCATTTCTTCAAGAAATTTACTGATATAGTTTTTAAATTTGAGCTGTATTTTC	4080	5101	CAGAGACAAGTCAAGATGATTTCACTGAAGTGTATGGGTATCTGTCTCTCAGATTAACC	5160
QY	4081	AAGCAGCTTTGCTTGGAAATCATTTGATATCCCTTTATTTTATCATTTCTTATTTTGA	4140	5161	CTTTTGTGCGCAGATACACTATTCAGGAGACATTTTGAATTTTATGGAGCTGTCAAAAGGAA	5220
DB	4081	AAGCAGCTTTGCTTGGAAATCATTTGATATCCCTTTATTTTATCATTTCTTATTTTGA	4140	5161	CTTTTGTGCGCAGATACACTATTCAGGAGACATTTTGAATTTTATGGAGCTGTCAAAAGGAA	5220
QY	4141	CAGAGAAATCATAGATCAAAAGCTTATCTCAACTTAACTTTGAGTCTTTTGGCACTG	4200	5221	TGAGTGCAGTGAATGACATGAAAGAGTCAATAGTCCGAATAACACATTCGACTTTTAAAG	5280
DB	4141	CAGAGAAATCATAGATCAAAAGCTTATCTCAACTTAACTTTGAGTCTTTTGGCACTG	4200	5221	TGAGTGCAGTGAATGACATGAAAGAGTCAATAGTCCGAATAACACATTCGACTTTTAAAG	5280
QY	4201	CATATTGATGGAACAGCTGTTTGTATATCCCTTTATTTTATCATTTCTTATTTTGA	4260	5281	AAACATCTTCAGAAAGCTGTAAAGAAACCTACCTGAGGAAATCAACACGAAAGTTGTGTTTG	5340
DB	4201	CATATTGATGGAACAGCTGTTTGTATATCCCTTTATTTTATCATTTCTTATTTTGA	4260	5281	AAACATCTTCAGAAAGCTGTAAAGAAACCTACCTGAGGAAATCAACACGAAAGTTGTGTTTG	5340
QY	4261	TGCTAGGAAGCTTACTGGCAATTTCAATATGGATATATTTTATCTGTAAGTTCCTTG	4320	5341	CTCTAAGTATGCTAGGGAATCCTCAGATTTACTTTTGTAGATGAACCACTACACAGGTATGG	5400
DB	4261	TGCTAGGAAGCTTACTGGCAATTTCAATATGGATATATTTTATCTGTAAGTTCCTTG	4320	5341	CTCTAAGTATGCTAGGGAATCCTCAGATTTACTTTTGTAGATGAACCACTACACAGGTATGG	5400
QY	4321	CTGTGGTTTTTGTGCTTATTTGTTTATGTTCCATCAGTATTTCTGTCTCACTATATTTGCTT	4380	5401	ATCCCAAAGCCAAAACAGCACATGTGGCGAGCAATTCGAACTGCAATTTTAAAAACAGAAAGC	5460
DB	4321	CTGTGGTTTTTGTGCTTATTTGTTTATGTTTCCATCAGTATTTCTGTCTCACTATATTTGCTT	4380	5401	ATCCCAAAGCCAAAACAGCACATGTGGCGAGCAATTCGAACTGCAATTTTAAAAACAGAAAGC	5460
QY	4381	CTTTTCACTTTTAAAGAAATTTT				

Db 5521 |||||CTATCATGTGTCTGGCGAGTTAAAGATGATCGGAACAGTACAAATCTATAAGAGTAAT 5580
QY 5581 |||||TTGGAAGAGGCTACTTTTGGAAATTAATTTGAAGGACTGGATAGAAAACCTTAGAAGTAG 5640
Db 5581 |||||TTGGAAGAGGCTACTTTTGGAAATTAATTTGAAGGACTGGATAGAAAACCTTAGAAGTAG 5640
QY 5641 ACGCCTTCAAGAGAAATTCAGTATATTTTCCAAATGCAAGCGCTCAGGAAAGTTT 5700
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Db 5701 CTTCTATTTTGGCTTATAAATTCCTTAAGGAGATGTTTTCAGTCCCTTTCACAAATCTTTT 5760
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QY 5821 CATTTGGAACAGGTTTGTAGAACTCACTAAGAACACAGAGGAGGAGATATAGTTG 5880
Db 5821 CATTTGGAACAGGTTTGTAGAACTCACTAAGAACACAGAGGAGGAGATATAGTTG 5880
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Db 5881 GAACCTTTAAACAGCACACTTTGGTGGAAACGACCAAGACGATAGAGTAGTATTTTGA 5940
QY 5941 TTTGTAATGTTGGCTGCTTACTGGGACTCTTTCTTTTTCACCTTAATTTTAACTTTGG 6000
Db 5941 TTTGTAATGTTGGCTGCTTACTGGGACTCTTTCTTTTTCACCTTAATTTTAACTTTGG 6000
QY 6001 TTTTAAAGAGTTTATTTGGAATGTTTAACTGAGAACCAAGACGCTTGAATTTTTC 6060
Db 6001 TTTTAAAGAGTTTATTTGGAATGTTTAACTGAGAACCAAGACGCTTGAATTTTTC 6060
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QY 6121 GTATAATTAAGTCAAGCTCAGTTTGTATTCAGATATATTCGAATATATATAGTTTGTATG 6180
Db 6121 GTATAATTAAGTCAAGCTCAGTTTGTATTCAGATATATATTCGAATATATATAGTTTGTATG 6180
QY 6181 TCATCTTTTTCACCATTCAGAAACAGTCTTCTGAAATTTGTAATTAAGGAATTTGTAAT 6240
Db 6181 TCATCTTTTTCACCATTCAGAAACAGTCTTCTGAAATTTGTAATTAAGGAATTTGTAAT 6240
QY 6241 AGAATAGTTTATTTTAAAGTTATCTTTTAAAGTTTATGCTTCTTTTAAATAAAGTACGTA 6300
Db 6241 AGAATAGTTTATTTTAAAGTTATCTTTTAAAGTTTATGCTTCTTTTAAATAAAGTACGTA 6300
QY 6301 ATGTTCCATCTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAGC 6360
Db 6301 ATGTTCCATCTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAGC 6360
QY 6361 AATGTGAAGTTTCTGCTTCTCTTTTAAATTTCTTAAATAAAGCCACTTTGAATGGAAGT 6420
Db 6361 AATGTGAAGTTTCTGCTTCTCTTTTAAATTTCTTAAATAAAGCCACTTTGAATGGAAGT 6420
QY 6421 TGTTCATCCGTAAAGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 6480
Db 6421 TGTTCATCCGTAAAGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 6480
QY 6481 AGTTATATCCACTAGTGGCAGTCAATTTGATCATAATAAAGTGAAT 6525
Db 6481 AGTTATATCCACTAGTGGCAGTCAATTTGATCATAATAAAGTGAAT 6525

RESULT 3
AAD33648
ID AAD33648 standard; cDNA; 6369 BP.
XX
AC AAD33648;

XX DT 01-JUL-2002 (first entry)
XX DE Human TRICH-3 cDNA.
XX KW Human; transporter and ion channel; TRICH-3; transport disorder; angina;
KW amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular disorder;
KW cardiac disorder; polymyositis; diabetes; neurological disorder; cancer;
KW depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease;
KW cell proliferated disorder; infertility; arteriosclerosis; gene therapy;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy;
KW myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension;
KW acquired immune deficiency syndrome; immunological disorder; scleroderma;
KW endocrine disorder; autoimmune thyroiditis; rheumatoid arthritis; goitre;
KW cardiac myopathy; amnesia; toxic myopathy; Addison's disease; infection;
KW epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease;
KW muscle disorder; stroke; dementia; anxiety; AIDS; asthma; cirrhosis;
KW gene; ss.
OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT CDS 1238..6166
FT /*tag= a
FT /product= "Human TRICH-3 protein"
XX PN WO200212340-A2.
XX PD 14-FEB-2002.
XX PF 01-AUG-2001; 2001WO-US024217.
XX PR 03-AUG-2000; 2000US-0223269P.
XX PR 10-AUG-2000; 2000US-0224456P.
XX PR 18-AUG-2000; 2000US-0226410P.
XX PR 25-AUG-2000; 2000US-0228140P.
XX PR 31-AUG-2000; 2000US-0230067P.
XX PR 08-SEP-2000; 2000US-0231434P.
XX (INCY-) INCYTE GENOMICS INC.
XX Yue H, Thornton M, Ramkumar J, Tang YT, Azimzai Y, Baughn ME;
PI Yang J, yao MG, Lal P, Walia NK, Gandhi AR, Hafalia AJA, Nguyen DB;
PI Patterson C, Elliott VS, Tribouley CM, Lu DAM, Xu Y, Reddy R;
PI Hernandez R, Borowsky ML, Lo TP, Lu Y, Policky JL, Greene BD;
PI Sanjanwala MS, Raumann BE, Burford N, Ison CH, Lee EA, Ding L;
PI Das D, Kallick DA, Khan FA, Seilhamer JJ;
XX WPI; 2002-206330/26.
XX P-PSDB; AAE21159.
XX
XX PT New human transporters and ion channels polypeptides and polynucleotides
XX for diagnosing, preventing or treating transport, neurological, muscle,
XX immunological and cell proliferative disorders.
XX
XX PS Claim 77; Page 203-205; 230pp; English.
XX
XX The invention relates to human transporter and ion channel polypeptides
XX designated TRICH and nucleic acid molecules encoding such polypeptides.
XX TRICH sequences are useful for diagnosis, treatment and prevention of
XX transport, muscle, neurological, immunological and cell proliferative
XX disorders. Transport disorders include akinesia, amyotrophic lateral
XX sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular
XX dystrophy, diabetes mellitus, diabetes insipidus, myasthenia gravis,
XX myocarditis, prostate cancer, cardiac disorders associated with transport
XX e.g. polymyositis, bradyarrhythmia, dermatomyositis, angina, neurological
XX disorders associated with transport e.g. amnesia, bipolar disorder,
XX depression, Tourette's disorder, schizophrenia, other disorders
XX associated with transport e.g. neurofibromatosis, sickle cell anaemia,
XX Wilson's disease, cataracts, infertility, hyperglycaemia, hypoglycaemia,
XX goitre, Cushing's disease, hypercholesterolaemia and cystinuria. Cell
XX proliferated disorders include cancer, actinic keratosis, cirrhosis,
XX arteriosclerosis, atherosclerosis, bursitis, hepatitis and psoriasis.

Neurological disorders include Alzheimer's, Pick's and Parkinson's disease, amyotrophic lateral sclerosis, epilepsy, stroke, Huntington's disease, multiple sclerosis, dementia and other extrapyramidal disorder, motor neuron disorder, prion disease, metabolic disease of the nervous system and other developmental disorders of the central nervous system, neuromuscular disorders, metabolic, endocrine and toxic myopathies, periodic paralysis, mental disorders including mood, anxiety; and immunological disorders include acquired immune deficiency syndrome (AIDS), adult respiratory distress syndrome, Addison's disease, allergies, asthma, atherosclerosis, osteoporosis, autoimmune haemolytic anaemia, autoimmune thyroiditis, Crohn's disease, atopic dermatitis, Grave's disease, glomerulonephritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, systemic sclerosis, ulcerative colitis, haemodialysis, uveitis; viral, bacterial, fungal, parasitic, protozoal, helminthic infections and trauma; and muscle disorders include cardiac myopathy, myocarditis, polymyositis, arrhythmias and hypertension. The TRICH polynucleotides are used in gene therapy. The present sequence is human TRICH-3 cDNA

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Query Match          93.8%; Score 6122.8; DB 6; Length 6369;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6127; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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Db	228	AAAAATGTTGATATTTTCTCTTAGCAGCGCTGCAACGAGGTTAGGTTTCAGGTCATAGTTT	287
Qy	61	CTACCCACATTTCTTTGAACTGAGTGTGTCATTTTATAGTTTATTTTTCAAAAACTTTTGCA	120
Db	288	CTACCCACATTTCTTTGAACTGAGTGTGTCATTTTATAGTTTATTTTTCAAAAACTTTTGCA	347
Qy	121	TACCTTTTGGTCTGCTGTTGTCAGTGAACAGTCTGAGTTTGACAGTTTGACAGTGGT	180
Db	348	TACCTTTTGGTCTGCTGTTGTCAGTGAACAGTCTGAGTTTGACAGTGGT	407
Qy	181	CTGTCGTGTTAGTTCAGTTTCTCAAGCCTTTGTACACTAATAGATTGCAATTATGTATG	240
Db	408	CTGTCGTGTTAGTTCAGTTTCTCAAGCCTTTGTACACTAATAGATTGCAATTATGTATG	467
Qy	241	TCCAGCTGGGAATTTATACAGGAATTAATAAACATTTTTTGAAGTGTCTTCTGAGCTC	300
Db	468	TCCAGCTGGGAATTTATACAGGAATTAATAAACATTTTTTGAAGTGTCTTCTGAGCTC	527
Qy	301	TCTTTCTATTGTTCCCGCTTCTACTTTTGTGCTTCCCTGTGGCTGTGTTTCTATCCTCC	360
Db	528	TCTTTCTATTGTTCCCGCTTCTACTTTTGTGCTTCCCTGTGGCTGTGTTTCTATCCTCC	587
Qy	361	AGCCAGAGAGCTAGTGTTTATTTTCTCCATTGTCTTACACACTGTGTGCAAGTGCACACAC	420
Db	588	AGCCAGAGAGCTAGTGTTTATTTTCTCCATTGTGTACACACTGTGTGCAAGTGCACACAC	647
Qy	421	CATATCCAGGGCCCAATGGTAGGAGGTAGAGAAAGAAAGCAAGGATGGCCTCATCC	480
Db	648	CATATCCAGGGCCCAATGGTAGGAGGTAGAGAAAGAAAGCAAGGATGGCCTCATCC	707
Qy	481	TCTTTACACGATAGTTCATTTGAAATAGAGAGAAAGGTTTTCTGCTCTCAGAGTGTGGCT	540
Db	708	TCTTTACACGATAGTTCATTTGAAATAGAGAGAAAGGTTTTCTGCTCTCAGAGTGTGGCT	767
Qy	541	GCACTAGGCTTTTGTGTTATGTAGTGTGGCCCTGTTACCATGGGATTTGCTTGATGTGGGG	600
Db	768	GCACTAGGCTTTTGTGTTATGTAGTGTGGCCCTGTTACCATGGGATTTGCTTGATGTGGGG	827
Qy	601	ATACAGGAGAAATTCAGAAAGAAAAAGATTGCTATTTCATTTCTCCCTCGAGCAATT	660
Db	828	ATACAGGAGAAATTCAGAAAGAAAAAGATTGCTATTTCATTTCTCCCTCGAGCAATT	887
Qy	661	AAGACCTCCCTTGCCCAATTCCTCAATTCOAAGCTAAGGCTTCTTCTGGAGCTGCCTCTGT	720
Db	888	AAGACCTCCCTTGCCCAATTCCTCAATTCOAAGCTAAGGCTTCTTCTGGAGCTGCCTCTGT	947

Db ||||| 2028 TTTCCTGGGTCTCTATATACAGTTTAAATTTCTTATGTCCTCTCTATGCGAGTCA 2087
QY ||||| 1861 TTGCGACAGCTCTCTTGTATTTCTCAAGTAGCAGCATTTGTGATATTTCTGCTTTTTT 1920
Db ||||| 2088 TTGCGACAGCTCTCTTGTATTTCTCAAGTAGCAGCATTTGTGATATTTCTGCTTTTTT 2147
QY ||||| 1921 TCCCTTATGGAATATCATCTGTATTTTGTCTTAAATGCTGACACCTCTTTTAAAAAAT 1980
Db ||||| 2148 TCCCTTATGGAATATCATCTGTATTTTGTCTTAAATGCTGACACCTCTTTTAAAAAAT 2207
QY ||||| 1981 CAAAAATGTGGAAATAGTTGAAATTTTGTACTGTGGCTTTTGGATTTATGCGCTTA 2040
Db ||||| 2208 CAAAAATGTGGAAATAGTTGAAATTTTGTACTGTGGCTTTTGGATTTATGCGCTTA 2267
QY ||||| 2041 TGAATATCCTCATAGAAAGTTTCCCAATCGTTAGTGGCTTTTCACTGCTTTCTGTC 2100
Db ||||| 2268 TGAATATCCTCATAGAAAGTTTCCCAATCGTTAGTGGCTTTTCACTGCTTTCTGTC 2327
QY ||||| 2101 ACTGTACTTTTGTGATTTGATTTGACAGGTCATGCAATTTAGAAGATTTTAAATGAAGTG 2160
Db ||||| 2328 ACTGTACTTTTGTGATTTGATTTGACAGGTCATGCAATTTAGAAGATTTTAAATGAAGTG 2387
QY ||||| 2161 CTTCAATTTCAAAATTTGACTGCGAGGCCATATCCTCTAATTTATCAATTTATCATGCTCA 2220
Db ||||| 2388 CTTCAATTTCAAAATTTGACTGCGAGGCCATATCCTCTAATTTATCAATTTATCATGCTCA 2447
QY ||||| 2221 CACTTAATAGTATATTTCTATGTCCTCTTGGCTGTCTATCTGATCAAGTCATCTCAGGGG 2280
Db ||||| 2448 CACTTAATAGTATATTTCTATGTCCTCTTGGCTGTCTATCTGATCAAGTCATCTCAGGGG 2507
QY ||||| 2281 AATTTGGCTTACGGAGATCATCTTTATATTTTCTGAGGCCCTTCATATTTGCTCAAGAGTA 2340
Db ||||| 2508 AATTTGGCTTACGGAGATCATCTTTATATTTTCTGAGGCCCTTCATATTTGCTCAAGAGTA 2367
QY ||||| 2341 AAGAAATTTATGAGGAGTTATCAGAGGCAATGTTAAATGGAATTTAGTTTGTAGTAA 2400
Db ||||| 2568 AAGAAATTTATGAGGAGTTATCAGAGGCAATGTTAAATGGAATTTAGTTTGTAGTAA 2627
QY ||||| 2401 TTATTGAGCCAGTTTCTCAGAAATTTGTAGAAAAGAGCCATAAGAAATTTAGTGTATTC 2460
Db ||||| 2628 TTATTGAGCCAGTTTCTCAGAAATTTGTAGAAAAGAGCCATAAGAAATTTAGTGTATTC 2687
QY ||||| 2461 AGAGACATACAGAAAGAGGTTGAAATGTCGGGCTTTGAGAAATTTGTCATTTGACA 2520
Db ||||| 2688 AGAGACATACAGAAAGAGGTTGAAATGTCGGGCTTTGAGAAATTTGTCATTTGACA 2747
QY ||||| 2521 TATATGAGGCTCAGATTTACTGCTTACTTTGGCCACAGTGGAAACAGGAAAGAGTACATTGA 2580
Db ||||| 2748 TATATGAGGCTCAGATTTACTGCTTACTTTGGCCACAGTGGAAACAGGAAAGAGTACATTGA 2807
QY ||||| 2581 TGAATATTTCTTGTGACTCTGCCACCTCTGATGGGTTTGCATCTATATAGACACA 2640
Db ||||| 2808 TGAATATTTCTTGTGACTCTGCCACCTCTGATGGGTTTGCATCTATATAGACACA 2867
QY ||||| 2641 GAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAATATGTCGCAATTTGTCACAGT 2700
Db ||||| 2868 GAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAATATGTCGCAATTTGTCACAGT 2927
QY ||||| 2701 TAGATATACATTTGTATGTTTGTAGATGAGAGAAATTTATCAATTTTGGCTTCAATCA 2760
Db ||||| 2928 TAGATATACATTTGTATGTTTGTAGATGAGAGAAATTTATCAATTTTGGCTTCAATCA 2987
QY ||||| 2761 AAGGATACAGCCAAATATATATCAAGAAAGTGCAGAGGTTTACTAGATTTTAGACA 2820
Db ||||| 2988 AAGGATACAGCCAAATATATATCAAGAAAGTGCAGAGGTTTACTAGATTTTAGACA 3047
QY ||||| 2821 TGCAGACTATCAAGATAACAGCTTAAATTTAAAGTGGTGTCAAAAAGAAAGAGTGT 2880
Db ||||| 3048 TGCAGACTATCAAGATAACAGCTTAAATTTAAAGTGGTGTCAAAAAGAAAGAGTGT 3107
QY ||||| 2881 CATTAGGAATTCGTCTTCTGGGACCCCAAGATCTGCTAGATGAACCAACAGCTG 2940

Db ||||| 3108 CATTAGGAATTCGTCTTCTGGGACCCAAAGATACTGCTGTAGATGAACCAACAGCTG 3167
QY ||||| 2941 GAATGGACCCCTCTCTCGACATATTTGTAATGTAATCTTTTAAAAATACAGAAAAGCCAAATC 3000
Db ||||| 3168 GAATGGACCCCTCTCTCGACATATTTGTAATGTAATCTTTTAAAAATACAGAAAAGCCAAATC 3227
QY ||||| 3001 GGGTGCAGAGTCTTCTGACTCTTCTCATGATGAAGTGCATCTTCTGAGATAGAAAG 3060
Db ||||| 3228 GGGTGCAGAGTCTTCTGACTCTTCTCATGATGAAGTGCATCTTCTGAGATAGAAAG 3287
QY ||||| 3061 CTGTGATATCACAAGAAATGCTGAATGTTGGTCTTCAATGTTCTCTCAAAAGTAAAT 3120
Db ||||| 3288 CTGTGATATCACAAGAAATGCTGAATGTTGGTCTTCAATGTTCTCTCAAAAGTAAAT 3347
QY ||||| 3121 GGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATTTTGTGCGCACAGAAATCTCTTT 3180
Db ||||| 3348 GGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATTTTGTGCGCACAGAAATCTCTTT 3407
QY ||||| 3181 CTTACCTGTTTAAACAAATATACCTGGAGCTACTTTTATACAGAAATGACCAACAC 3240
Db ||||| 3408 CTTCACTGGTTAAACAAATATACCTGGAGCTACTTTTATACAGAAATGACCAACAC 3467
QY ||||| 3241 TTGTGTATAGTCTTGCCTTTCAAGGACATGACAAATTTTCAAGTTTGTCTGCGCTAG 3300
Db ||||| 3468 TTGTGTATAGTCTTGCCTTTCAAGGACATGACAAATTTTCAAGTTTGTCTGCGCTAG 3527
QY ||||| 3301 ACAGTCAATCAAAATTTGGGTGTCATTTCTTATGGTGTTCATTTCCATGACAGCTTTGGAAGAG 3360
Db ||||| 3528 ACAGTCAATCAAAATTTGGGTGTCATTTCTTATGGTGTTCATTTCCATGACAGCTTTGGAAGAG 3587
QY ||||| 3361 TATTTTAAAGCTAGAGTTGAAGCAAAATTTGACCAAGCAGATTTAGTGTATTTACTC 3420
Db ||||| 3588 TATTTTAAAGCTAGAGTTGAAGCAAAATTTGACCAAGCAGATTTAGTGTATTTACTC 3647
QY ||||| 3421 AGCAGCACCTGGAGGAGAAATGGATTTCAAAATCTTTTGTGAAATGGAACAGAGCTTAC 3480
Db ||||| 3648 AGCAGCACCTGGAGGAGAAATGGATTTCAAAATCTTTTGTGAAATGGAACAGAGCTTAC 3707
QY ||||| 3481 TTATTTCTTTGAAACCAAGGCTTCTTAGTGAGCACCAGCTTTGGAAACACACAGA 3540
Db ||||| 3708 TTATTTCTTTGAAACCAAGGCTTCTTAGTGAGCACCAGCTTTGGAAACACACAGA 3767
QY ||||| 3541 TGTATACATAGCAAAAGTTTCATTTCTTTACCTTGAACCTGAAAGCTGAAATTAATCAGTGAGAT 3600
Db ||||| 3768 TGTATACATAGCAAAAGTTTCATTTCTTTACCTTGAACCTGAAAGCTGAAATTAATCAGTGAGAT 3827
QY ||||| 3601 CAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTGGTTCATC 3660
Db ||||| 3828 CAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTGGTTCATC 3887
QY ||||| 3661 ACTCTTTTAAAAATGCTGTTTCCCATCAAACTTGTTCAGACTTATATTTTCTAAAAAC 3720
Db ||||| 3888 ACTCTTTTAAAAATGCTGTTTCCCATCAAACTTGTTCAGACTTATATTTTCTAAAAAC 3947
QY ||||| 3721 CTGAGACAAACCAACATAAATAACAAAGCTGCTTCTTCTTCAAAATTTCTGCTGACTCAG 3780
Db ||||| 3948 CTGAGACAAACCAACATAAATAACAAAGCTGCTTCTTCTTCAAAATTTCTGCTGACTCAG 4007
QY ||||| 3781 ATATCAGTGATCTTATTTAGCTTTTTCACAGCCAGAACATAATGTTGAGCTGATTAATG 3840
Db ||||| 4008 ATATCAGTGATCTTATTTAGCTTTTTCACAGCCAGAACATAATGTTGAGCTGATTAATG 4067
QY ||||| 3841 ACAGTGAATGATCGTGGCTCCCATAGTGGCTTTTAAATGTTGATGCTGATTAATG 3900
Db ||||| 4068 ACAGTGAATGATCGTGGCTCCCATAGTGGCTTTTAAATGTTGATGCTGATTAATG 4127
QY ||||| 3901 AGGACTATGTTTGGAGCTGTTTCAACAGTACTATGTTTATTTCTTTACCTATATTAG 3960
Db ||||| 4128 AGGACTATGTTTGGAGCTGTTTCAACAGTACTATGTTTATTTCTTTACCTATATTAG 4187
QY ||||| 3961 TGAATATCATTAGTAACTACTCTTTTATCATTTAAATGTTGACTGAAACCAATCCAGATCT 4020
Db ||||| 4188 TGAATATCATTAGTAACTACTCTTTTATCATTTAAATGTTGACTGAAACCAATCCAGATCT 4247

QY 4021 GGAGTACCCCATCTCTTTCAAGAAATTTACTGATATAGTTTTTAAATTTGAGCTGTATTTTC 4080
DB 4248 GGAGTACCCCATCTCTTTCAAGAAATTTACTGATATAGTTTTTAAATTTGAGCTGTATTTTC 4307
QY 4081 AAGCAGCTTTGCTTTGGAATCATTTGTTACTGCAATGCCACCTTACTTTGGCCATGGAATAAG 4140
DB 4308 AAGCAGCTTTGCTTTGGAATCATTTGTTACTGCAATGCCACCTTACTTTGGCCATGGAATAAG 4367
QY 4141 CAGAGATCATAGATCAAGAGCTTATATCTCAACTTAAACCTTCAAGTCTTTTGGCCATCTG 4200
DB 4368 CAGAGATCATAGATCAAGAGCTTATATCTCAACTTAAACCTTCAAGTCTTTTGGCCATCTG 4427
QY 4201 CATATTTGATTTGGAACAAGCTTTGTTGATATCCCTTATTTTATCATTTCTTATTTTGA 4260
DB 4428 CATATTTGATTTGGAACAAGCTTTGTTGATATCCCTTATTTTATCATTTCTTATTTTGA 4487
QY 4261 TGCTAGGAAGCTTACTGCAATTCATTATATGATATATATTTTATCTGTAAGATTCCTTG 4320
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DB 4668 CAGGCTGCTTTGATTTGCAATCTAGTAAATTAACCTTTCTTTATGGGATACACAAATTCGA 4727
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DB 4788 TTTCTTTCAATAAGATTTCTTTGGAAGATGTACGAAATAATGTGGAACACCTATATATCCAT 4847
QY 4621 GGGATAGCTTTTCACTAGCTGTTATATCGCTTACCTGCACTGTTACTGTGGATTTTCC 4680
DB 4848 GGGATAGCTTTTCACTAGCTGTTATATCGCTTACCTGCACTGTTACTGTGGATTTTCC 4907
QY 4681 TCTTCAATATCTATGAGAAAATAATGAGGCGAGATCAATTAAGAAAAGATCCCTTTTCA 4740
DB 4908 TCTTCAATATCTATGAGAAAATAATGAGGCGAGATCAATTAAGAAAAGATCCCTTTTCA 4967
QY 4741 GAAACCTTTCAACGAAGTCTTAAATAGGAAGCTTCCAGAACCCACGACAAATCAGGATG 4800
DB 4968 GAAACCTTTCAACGAAGTCTTAAATAGGAAGCTTCCAGAACCCACGACAAATCAGGATG 5027
QY 4801 AAGATGAAGATGTCAAAGCTCAAAGCTAAAAGGTCAAAAGAGCTGATGGGTTGCCAGTGT 4860
DB 5028 AAGATGAAGATGTCAAAGCTCAAAGCTAAAAGGTCAAAAGAGCTGATGGGTTGCCAGTGT 5087
QY 4861 GTGAGGAGAACCATTCATTTATGTTGTCAGCAATTTTGCAATAAAGATATGATGACAGAAAG 4920
DB 5088 GTGAGGAGAACCATTCATTTATGTTGTCAGCAATTTTGCAATAAAGATATGATGACAGAAAG 5147
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DB 5148 ATTTTCTCTTTTCAAGAAAAGTAAAGAAAGTGGCAACTTAAATACATCTCTTTCTGTGTGA 5207
QY 4981 AAAAAAGGAGATCTTAGGACTTATTTGGTCCAAATGGTGGCCAAAGCAATATTATTA 5040
DB 5208 AAAAAAGGAGATCTTAGGACTTATTTGGTCCAAATGGTGGCCAAAGCAATATTATTA 5267
QY 5041 ATATTTCTGGTGGTATTTGAACCAACTTCAGGCCAGGTATTTTATGAGATATTCTT 5100
DB 5268 ATATTTCTGGTGGTATTTGAACCAACTTCAGGCCAGGTATTTTATGAGATATTCTT 5327

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DB 5328 CAGAGACAAGTGAAGATGATGATTTCACTGAAGTGTATGGTTACTGTCTCAGATAAAC 5387
QY 5161 CTTTGTGGCCAGATACTACTATTTGAGGAACATTTTGAATTTATGAGCTGTCAAAGAA 5220
DB 5388 CTTTGTGGCCAGATACTACTATTTGAGGAACATTTTGAATTTATGAGCTGTCAAAGAA 5447
QY 5221 TGAGTGCAGAGTGAAGTGAAGAAAGTCAATAAGTCCGAATTAACACATGCTGATTTTAAAG 5280
DB 5448 TGAGTGCAGAGTGAAGTGAAGAAAGTCAATAAGTCCGAATTAACACATGCTGATTTTAAAG 5507
QY 5281 AAACATCTTTCAGAAAGCTGTAAAGAAACCTACCTGAGGAATCAAAAGAAAGTTGTTTTG 5340
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QY 5401 ATCCCAAGCCAAAACAGCACATGTGCGAGCAATTTGCAACTGTCATTTTAAACACAGAAAG 5460
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QY 5461 GGGCTGCTATTTCTGACCACTCATATATGGAGGCGCAGAGCTCTCTGTGATCGAGTAG 5520
DB 5688 GGGCTGCTATTTCTGACCACTCATATATGGAGGCGCAGAGCTCTCTGTGATCGAGTAG 5747
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QY 5641 ACGCCTTCAAAGAGAAATTCAGTATATTTTCCCAATTCGAAGCGGTGAGGAAAGTTTTT 5700
DB 5868 ACGCCTTCAAAGAGAAATTCAGTATATTTTCCCAATTCGAAGCGGTGAGGAAAGTTTTT 5927
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DB 5928 CTTCTATTTTGGCTTATAAAATTCCTAAGAAAGATGTTTCAGTCCCTTTTCACAATCTTTTT 5987
QY 5761 TTAAAGTGAAGAGCTAAACATGCTTTTGGCAATGAAGAAATATAGCTTTTCTCAAGCAA 5820
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QY 5821 CATTTGAAACAGGTTTTTTGTAGAACTCACTAAAGAACAGAGGAGGAAGATAATAGTTGTG 5880
DB 6048 CATTTGAAACAGGTTTTTTGTAGAACTCACTAAAGAACAGAGGAGGAAGATAATAGTTGTG 6107
QY 5881 GAACTTTAAACAGCACTTTTGGTGGGAACGAAACACAGAGAGATAGATAGTATTTTGA 5940
DB 6108 GAACTTTAAACAGCACTTTTGGTGGGAACGAAACACAGAGAGATAGATAGTATTTTGA 6167
QY 5941 TTTGATTTGTTGGTCTGCTTACTGGGACTTCTTTCTTTTTCACITTAATTTTAACTTTGG 6000
DB 6168 TTTGATTTGTTGGTCTGCTTACTGGGACTTCTTTCTTTTTCACITTAATTTTAACTTTGG 6227
QY 6001 TTTTAAAGAGTTTTTATTTGGAATGTTAACTGGAGAACCAAGAACCGCACTTGAATTTTTC 6060
DB 6228 TTTTAAAGAGTTTTTATTTGGAATGTTAACTGGAGAACCAAGAACCGCACTTGAATTTTTC 6287
QY 6061 TAAGCTCCTTAAATTTGAATGCTGTGTGTTGTTTTGTTTTCTTTTAAATAAAACGTAT 6120
DB 6288 TAAGCTCCTTAAATTTGAATGCTGTGTGTTGTTTTGTTTTCTTTTAAATAAAACGTAT 6347
QY 6121 GTATAATTAAGTGAA 6135
DB 6348 GTATAATTAAGTGAA 6362

[illegible]

QY 181 CTGTCCTTAGTTTCAGTTTCTCAAGCCTTTGTGCACACTAATAGGATTTATGTATG 240
Db 408 CTGTCCTTAGTTTCAGTTTCTCAAGCCTTTGTGCACACTAATAGGATTTATGTATG 467
QY 241 TCCAGCTTGGGAATATTATACAGGAATTAATAAACAACCTTTTAGAGTCTTTCTGAGCTC 300
Db 468 TCCAGCTTGGGAATATTATACAGGAATTAATAAACAACCTTTTAGAGTCTTTCTGAGCTC 527
QY 301 TCTTTCTATTGTTCCCTCTTCTACTTTTGTCTTCCCTGTGGCTGTGTTTCTATCTCTCC 360
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QY 421 CATATCAGGGCCCAATGGTAGGAGGTAGAGAGAAAGCAAAAGGAATTTGGCCTCATCC 480
Db 648 CATATCAGGGCCCAATGGTAGGAGGTAGAGAGAAAGCAAAAGGAATTTGGCCTCATCC 707
QY 481 TCTTACACAGATAGTTCATTTGAATAGAGAGAAAGGTTTCTCTGCTCAGAGTGTGGCT 540
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QY 541 GCACTAGCTTTTGTACTGTAGTCTGGCCCTGTACCATGGGATTTGCTTGCATGTGGG 600
Db 768 GCACTAGCTTTTGTACTGTAGTCTGGCCCTGTACCATGGGATTTGCTTGCATGTGGG 827
QY 601 ATACAGAGGAATTCAGAAAAGAAAAGATTTCTCTATTTCTACATTTCTCCCTGAGCAT 660
Db 828 ATACAGAGGAATTCAGAAAAGAAAAGATTTCTCTATTTCTACATTTCTCCCTGAGCAT 887
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QY 841 CCATGCATCTGTCAGCTTTCTTAAGAGAGACAGCTTGGAGTATGCTTAATCCATCTTAC 900
Db 1068 CCATGCATCTGTCAGCTTTCTTAAGAGAGACAGCTTGGAGTATGCTTAATCCATCTTAC 1127
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Db 1368 TTTGGTTAATATTATTTAGCATGATCCCAATTAAGAAATATGAAGAGTGCCTAATA 1427
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Db 1968 AAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATCTGCTTTTGGC 2027
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Db 2028 TTTCTCGGTTCTCTATATACAAAGTTAAATTTTCTTATGTCCTTTCTTATGGAGTCA 2087
QY 1861 TTGCGACAGCTTTTGTGTTATTTCTCAAGTAGCAGCATTTGATATTTCTGCTTTTT 1920
Db 2088 TTGCGACAGCTTTTGTGTTATTTCTCAAGTAGCAGCATTTGATATTTCTGCTTTTT 2147
QY 1921 TCTTTATGGATATCATCTGATTTTGTCTTAAATGCTGACACCTCTTTTAAAAAAT 1980
Db 2148 TCTTTATGGATATCATCTGATTTTGTCTTAAATGCTGACACCTCTTTTAAAAAAT 2207
QY 1981 CAAAAATGTTGGGAATGATTTGAAATTTTGTACTGTGCTTTTGGATTTATTTGGCCTTA 2040
Db 2208 CAAAAATGTTGGGAATGATTTGAAATTTTGTACTGTGCTTTTGGATTTATTTGGCCTTA 2267
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QY 2161 CTTTCATTTTCAAAATTTGACTGCGAGGCCATATCTCTAATTTATTAATTTATCATCTCA 2220
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QY 2221 CACTTAATAGTATTTCTATGCTCTCTGCTGTCTATCTTGTATCAAGTCATTTCCAGGGG 2280
Db 2448 CACTTAATAGTATTTCTATGCTCTCTGCTGTCTATCTTGTATCAAGTCATTTCCAGGGG 2507
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Db 2508 AATTTGCTTTACGGAGATCATCTTTATATTTTCTGAAGCTTCATATTTGTCACAGATA 2567
QY 2341 AAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAAATGGAAATATTAGTTTTAGTGA 2400

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2461 AGAAGACATACAGAAAGAGGTTGAAAATGTTGAGGCTTTTGAGAAATTTGTCAATTTGACA 2520
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2521 TATATGAGGTCAGATTACTGCTTACTTGGCCACAGTGGACAGAAAGAGTACATTTGA 2580
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2928 TAGATATACATTTGATGTTTGGACAGTAGAAGAAAATTTATCAATTTTGGCTTCAATCA 2987
2761 AAGGATACCCAGCAACAATATAACAAAGAGTCAGAAAGTTTACTAGATTTAGACA 2820
2988 AAGGATACCCAGCAACAATATAACAAAGAGTCAGAAAGTTTACTAGATTTAGACA 3047
2821 TCAGACTATCAAGATACCAAGCTTAAAGATTTAAGTGGTGTCAAAAAGAGAGCTGT 2880
3048 TGCAACTATCAAGATACCAAGCTTAAAGATTTAAGTGGTGTCAAAAAGAGAGCTGT 3107
2881 CATTAGGAATTTGCTTTCTTGGGAACCCAAAGATACTGCTGATGAAACCAACAGCTG 2940
3108 CATTAGGAATTTGCTTTCTTGGGAACCCAAAGATACTGCTGATGAAACCAACAGCTG 3167
2941 GAATGACCCCTGTTCTCGACATATTTGATGAATTTTAAATACAGAAAGCAATC 3000
3168 GAATGACCCCTGTTCTCGACATATTTGATGAATTTTAAATACAGAAAGCAATC 3227
3001 GGGTGACAGTTTCAGTACTCAATTTATGATGAAGCTGACATTTCTGACAGATAGAAAG 3060
3228 GGGTGACAGTTTCAGTACTCAATTTATGATGAAGCTGACATTTCTGACAGATAGAAAG 3287
3061 CTGTGATATCACAGGAATGCTGAATGTTGTTGTTCTTCAATGTTCTCAAAAGTAAAT 3120
3288 CTGTGATATCACAGGAATGCTGAATGTTGTTGTTCTTCAATGTTCTCAAAAGTAAAT 3347
3121 GGGGGATCGCTACCCCTGAGCATGTACATAGACAAATATTGTCACAGAAATCTCTTT 3180
3348 GGGGGATCGCTACCCCTGAGCATGTACATAGACAAATATTGTCACAGAAATCTCTTT 3407
3181 CTTCACTGTTTAAACAAATATACCTGGAGCTACTTTATACAAAGATAGCAACAAAC 3240
3408 CTTCACTGTTTAAACAAATATACCTGGAGCTACTTTATACAAAGATAGCAACAAAC 3467
3241 TTGTGTATAGCTTGCCTTTTCAAGGACATGGACAAATTTTCAAGTGTGTTTCTGCGCTAG 3300
3468 TTGTGTATAGCTTGCCTTTTCAAGGACATGGACAAATTTTCAAGTGTGTTTCTGCGCTAG 3527
3301 ACAGTCATTTCAAAATTTGGGTGTCTTTCTATGTTGTTTCCATGACGATTTTGAAGAGC 3360
3528 ACAGTCATTTCAAAATTTGGGTGTCTTTCTATGTTGTTTCCATGACGATTTTGAAGAGC 3587
3361 TATTTTAAAGCTAGAAAGTTGAAGCAAGAAATTTGAACCAAGCAATTTATGTTATCTC 3420
3588 TATTTTAAAGCTAGAAAGTTGAAGCAAGAAATTTGAACCAAGCAAGCTCAG----- 3629
3421 AGCAGCCACTGGAGGAAGAAATGGAATTTCAAAATCTTTTATGAATGGAACAGAGCTTAC 3480

3630 ----- 3629
3481 TTATTCTTTCTGAAACCAAGCTTCTCTAGTGAGCACCATGAGCCTTTGGAACCAACAGA 3540
3630 ----- 3629
3541 TGATACATAGCAAGTTTCAITCTTTACCTTGAACGTGAAGTAATCAGTGAGAT 3600
3630 ----- 3629
3601 CAGTGTGCTTCTGCTTTTAAATTTTTTACAGTTCAGATTTTTTATGTTTGGTTTCACTC 3660
3630 -----GTTGCTTCTGCTTTTAAATTTTTTACAGTTCAGATTTTTTATGTTTGGTTTCACTC 3685
3661 ACTCTTTTAAATAGCTGTGGTTCATCAAACTGTTCCAGCTTATATTTTCTTAAAC 3720
3686 ACTCTTTTAAATAGCTGTGGTTCATCAAACTGTTCCAGCTTATATTTTCTTAAAC 3745
3721 CTGAGACAAACACATATAACAAACCAAGTCTGCTTCTTCAAAATTTCTGCTGACTCAG 3780
3746 CTGAGACAAACACATATAACAAACCAAGTCTGCTTCTTCAAAATTTCTGCTGACTCAG 3805
3781 ATATCAGTGTCTTTATAGCTTTTCAAGGCCAGAACATAATGGTGACGATTAATG 3840
3806 ATATCAGTGTCTTTATAGCTTTTCAAGGCCAGAACATAATGGTGACGATTAATG 3865
3841 ACAGTACTATGATCGGTGGCTCCCATAGTGGCTTTAAATGTGATGATTCAGAAA 3900
3866 ACAGTACTATGATCGGTGGCTCCCATAGTGGCTTTAAATGTGATGATTCAGAAA 3925
3901 AGGACTATGTTTGTGAGCTGTTTCAACAGTACTATGTTTATTCTTTACCTATATTAG 3960
3926 AGGACTATGTTTGTGAGCTGTTTCAACAGTACTATGTTTATTCTTTACCTATATTAG 3985
3961 TGAATATCATTAGTACTATCTTTATCAATTAATGTGACTGAAACCAATCCAGATCT 4020
3986 TGAATATCATTAGTACTATCTTTATCAATTAATGTGACTGAAACCAATCCAGATCT 4045
4021 GGAGTACCCCATTTCTTCAAGAAATTTACTGATAGTGTTTTAAATTTGAGCTGATTTTC 4080
4046 GGAGTACCCCATTTCTTCAAGAAATTTACTGATAGTGTTTTAAATTTGAGCTGATTTTC 4105
4081 AAGCAGCTTTGCTTGGAAATCAITTTGTTACTGCAATGCCACCTTACTTTGCCATGGAAAATG 4140
4106 AAGCAGCTTTGCTTGGAAATCAITTTGTTACTGCAATGCCACCTTACTTTGCCATGGAAAATG 4165
4141 CAGAGATCATAGATCAAGCTTATCACTCAACTTAAACCTTTTCCAGCTCTTTTGGCCATCTG 4200
4166 CAGAGATCATAGATCAAGCTTATCACTCAACTTAAACCTTTTCCAGCTCTTTTGGCCATCTG 4225
4201 CATATTGGATTGACAAAGCTGTTGTTGATATCCCTTATTTTATCAITCTTTATTTTGA 4260
4226 CATATTGGATTGACAAAGCTGTTGTTGATATCCCTTATTTTATCAITCTTTATTTTGA 4285
4261 TGCTAGAACTTACTGGCAATTTCAATGATGATATTTTATATCTGTAAGTCTCTG 4320
4286 TGCTAGAACTTACTGGCAATTTCAATGATGATATTTTATATCTGTAAGTCTCTG 4345
4321 CTGTGGTTTTTGGCTTATTTGGTTATGTTCCATCAGTATTTCTGTTCACTTATTTGCTT 4380
4346 CTGTGGTTTTTGGCTTATTTGGTTATGTTCCATCAGTATTTCTGTTCACTTATTTGCTT 4405
4381 CTTTCACTTTTAAAGAAAATTTTAAATACCAAGAAATTTTGGTCAATTTATCTGCTG 4440
4406 CTTTCACTTTTAAAGAAAATTTTAAATACCAAGAAATTTTGGTCAATTTATCTGCTG 4465
4441 CAGGTTGCTGCTGATTTGCAATCACTGAAATTTTGGTCAATTTATCTGCTG 4500
4466 CAGGTTGCTGCTGATTTGCAATCACTGAAATTTTGGTCAATTTATCTGCTG 4525
4501 CTATTCTTCAATGCTTTTGTATCATCATTCCTATCCACTTTCTAGGTTGCTG 4560
4526 CTATTCTTCAATGCTTTTGTATCATCATTCCTATCCACTTTCTAGGTTGCTG 4585

DR	P-PSDB; ABG72424.	QY	1474	CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG	1533
XX		Db	577	CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG	636
PT	Novel isolated ATP binding cassette transporter family polypeptide,	QY	1534	TTTTTACAAGCATCCATAGATGCTGCCATTTATACAGTTGAAGACCAATGTTTCTCTTTGA	1593
PT	ABCA5 transporter expression or activity.	Db	637	TTTTTACAAGCATCCATAGATGCTGCCATTTATACAGTTGAAGACCAATGTTTCTCTTTGA	696
PS	Claim 2; Page 39-42; 52pp; English.	QY	1594	AGGAGCTGGAGTCAACTAAAGCTGTTTATATGGGAGAACTGCTGTGTAGAAATAGATA	1653
XX	The invention describes an isolated ATP binding cassette (ABC)	Db	697	AGGAGCTGGAGTCAACTAAAGCTGTTTATATGGGAGAACTGCTGTGTAGAAATAGATA	756
CC	transporter family polypeptide (I), designated ABCA5. (I) or the	QY	1654	CCTTTCCCAGGAGTAATTTTAAATACCTAGTTATAGCATTTTCCCTTTTGGATACT	1713
CC	polynucleotide encoding it (II) are useful as targets for developing	Db	757	CCTTTCCCAGGAGTAATTTTAAATACCTAGTTATAGCATTTTCCCTTTTGGATACT	816
CC	modulating agents to regulate a variety of cellular processes,	QY	1714	TTTTTGGCAATTCATATCGTAGCAGAAAAAATAAAAGAAATTTTAAAGATAA	1773
CC	particularly the transport of neurotoxic molecules, e.g., beta-amyloid	Db	817	TTTTTGGCAATTCATATCGTAGCAGAAAAAATAAAAGAAATTTTAAAGATAA	876
CC	peptide (Abeta), across cell membranes or, e.g., the blood brain barrier	QY	1774	TGGGACTTCATGATACCTGCTTTTGGCTTTTCCCTGGGTTCTTCTATATACAAGTTTAATTT	1833
CC	(BBB), as targets for developing modulating agents of multi-drug	Db	877	TGGGACTTCATGATACCTGCTTTTGGCTTTTCCCTGGGTTCTTCTATATACAAGTTTAATTT	936
CC	resistance, as diagnostic and therapeutic tools, or to treat disorders	QY	1834	TTCTTATGTCCCTTCTTATGGCAGTCATTCGCACAGCTTCTTTTGTATTTTCTCAAGTA	1893
CC	associated with aberrant or unwanted ABCA5 transporter expression or	Db	937	TTCTTATGTCCCTTCTTATGGCAGTCATTCGCACAGCTTCTTTTGTATTTTCTCAAGTA	996
CC	activity. (I), (II) or a host cell (III) expressing (II) are useful in	QY	1894	GCAGCATTTGATATTTCTGCTTTTCTTCTTATGGATATCACTGTATTTTGTCTT	1953
CC	screening assays, detection assays (e.g., chromosomal mapping, tissue	Db	997	GCAGCATTTGATATTTCTGCTTTTCTTCTTATGGATATCACTGTATTTTGTCTT	1056
CC	typing, forensic biology), predictive medicine (e.g., diagnostic assays,	QY	1954	TAATGTCTGACACCTCTTTTAAAAAATCAAAACATGTGGAAATAGTTGAATTTTGTGA	2013
CC	prognostic assays, monitoring clinical trials and pharmacogenomics), and	Db	1057	TAATGTCTGACACCTCTTTTAAAAAATCAAAACATGTGGAAATAGTTGAATTTTGTGA	1116
CC	in methods of treatment (e.g., therapeutic and prophylactic). (I) or	QY	2014	CTGTGCTTTTGGATTTATGGCTTTATGATATCTCTATAGAAAGTTTCCCAATCTG	2073
CC	(III) are useful as reagents or targets in assays applicable to treatment	Db	1117	CTGTGCTTTTGGATTTATGGCTTTATGATATCTCTATAGAAAGTTTCCCAATCTG	1176
CC	and diagnosis of ABCA5-mediated or related disorders. (I) is useful to	QY	2074	TAGTGTGCTTTTTCAGTCCCTTCTGTCAGTCTTCTTCTGTTGTTGTTTGCACAGTCA	2133
CC	screen for naturally occurring ABCA5 substrates; to screen for drugs or	Db	1177	TAGTGTGCTTTTTCAGTCCCTTCTGTCAGTCTTCTTCTGTTGTTTGCACAGTCA	1236
CC	compounds which modulate ABCA5 activity; as a bait protein in a yeast two	QY	2134	TGCATTTAGAAGATTTTAAATGAAGTGCTTCAATTTTCAAATTTGACTGCAGGCCCATATC	2193
CC	-hybrid or three-hybrid assay; and to identify other proteins which bind	Db	1237	TGCATTTAGAAGATTTTAAATGAAGTGCTTCAATTTTCAAATTTGACTGCAGGCCCATATC	1296
CC	to or interact with ABCA5. (II) is useful in: gene therapy; to detect	QY	2194	CTCTAATTTATCAATTAATCATGCTCACACTTAATAGTATATTTCTATGCTCTTGGCTG	2253
CC	ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5	Db	1297	CTCTAATTTATCAATTAATCATGCTCACACTTAATAGTATATTTCTATGCTCTTGGCTG	1356
CC	activity; to locate gene regions associated with genetic disease or to	QY	2254	CTCTAATTTATCAATTAATCATGCTCACACTTAATAGTATATTTCTATGCTCTTGGCTG	2313
CC	associate ABCA5 with the disease, to identify an individual from a minute	Db	1357	CTCTAATTTATCAATTAATCATGCTCACACTTAATAGTATATTTCTATGCTCTTGGCTG	1416
CC	biological sample (tissue typing), and to aid in forensic identification	QY	2314	TGAAGCTTTCATATTTGGTCTAAAGAGTAAAGAAATTTATGAGAGTTATCAGAGGCAATG	2373
CC	of the biological sample. This sequence encodes a novel human ATP binding	Db	1417	TGAAGCTTTCATATTTGGTCTAAAGAGTAAAGAAATTTATGAGAGTTATCAGAGGCAATG	1476
CC	cassette (ABC) A5 transporter	QY	2374	TTAATGGAATATTTAGTGTGAAATTTATGAGCCAGTTTCTTCAAGAAATTTGTAGGAA	2433
XX		Db	1477	TTAATGGAATATTTAGTGTGAAATTTATGAGCCAGTTTCTTCAAGAAATTTGTAGGAA	1536
SQ	Sequence 5475 BP; 1705 A; 917 C; 1048 G; 1804 T; 0 U; 1 Other;	QY	2434	AAGAAGCCATAGAATTTAGTGTGTTTTCAGAAGACATACAGAAGAGGGTGAATGTGG	2493
	Query Match 82.3%; Score 5373.2; DB 10; Length 5475;	Db	1537	AAGAAGCCATAGAATTTAGTGTGTTTTCAGAAGACATACAGAAGAGGGTGAATGTGG	1596
	Best Local Similarity 99.9%; Pred. No. 0;	QY	2494	AGGCTTTGAGAAATTTGTCTATTTGACATATATGAGGGTTCAGATTACTGCTTACTTGGCC	2553
	Matches 5375; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Db	1597	AGGCTTTGAGAAATTTGTCTATTTGACATATATGAGGGTTCAGATTACTGCTTACTTGGCC	1656
QY	994 AGGTTTATTCAGAAACATGTCACCTGCAATAGGAGGTAGGAGTTTGGAGACAGCA	QY	2554	ACAGTGGACAGGAAAGAGTACATTTGATGAATATTTTGTGGAGCTCTGCCACCTTCTG	2613
Db	97 AGGTTTATTCAGAAACATGTCACCTGCAATAGGAGGTAGGAGTTTGGAGACAGCA				
QY	1054 GAACCTTCTACTGAAGATTTACTTAATTAATGAGAACCAAAAGAGTAGTTTCAGG				
Db	157 GAACCTTCTACTGAAGATTTACTTAATTAATGAGAACCAAAAGAGTAGTTTCAGG				
QY	1114 AAATCTTTTCCACTATTTTATTTTATTTTGGTTAATATTAATAGCATGATGCATCAA				
Db	217 AAATCTTTTCCACTATTTTATTTTGGTTAATATTAATAGCATGATGCATCAA				
QY	1174 ATAAGAAATATGAGAGTGGCTTATATAGTACTCACTTATGAGTGTGAGTGTCTCTTT				
Db	277 ATAAGAAATATGAGAGTGGCTTATATAGTACTCACTTATGAGTGTGAGTGTCTCTTT				
QY	1234 CTAATCTAATTTCTTGGATATCTCCAGTGACTAATATTAACAGCAGCATCATGCAGAAAG				
Db	337 CTAATCTAATTTCTTGGATATCTCCAGTGACTAATATTAACAGCAGCATCATGCAGAAAG				
QY	1294 TGTCTACTGATCATCTACCTGATGTCATTAATTAATGAGAAATATACAAATGAAAGAAA				
Db	397 TGTCTACTGATCATCTACCTGATGTCATTAATTAATGAGAAATATACAAATGAAAGAAA				
QY	1354 TGTTCATCTCCAGTCTCTCTAAGCCGAGCAACTTTGTAGTGTGTTTCAAAGACTCCA				
Db	457 TGTTCATCTCCAGTCTCTCTAAGCCGAGCAACTTTGTAGTGTGTTTCAAAGACTCCA				
QY	1414 TGTCTCTATGAACCTCGTTTTTTTCTCTGATATGATTTCCAGTATCTTCTATTTATGATTT				
Db	517 TGTCTCTATGAACCTCGTTTTTTTCTCTGATATGATTTCCAGTATCTTCTATTTATGATTT				

QY	4774	TTCCAGAACCAACAGACCAATGAGGATGAAGATGAAGATGTCAAAGCTGAAGACTAAAGG	4833	QY	5854	AACAAGAGGAGGAGATATAGTTGTGGAACTTTAAACAGCACACCTTTGGTGGAAACGAA	5913
Db	3877	TTCCAGAACCAACAGACCAATGAGGATGAAGATGAAGATGTCAAAGCTGAAGACTAAAGG	3936	Db	4957	AACAAGAGGAGGAGGAGATATAGTTGTGGAACTTTAAACAGCACACCTTTGGTGGAAACGAA	5016
QY	4834	TCAAGAGCTGATGGGTGCCAGTGTGTGAGGAGAAACCATCCATTTATGGTGCAGCAATT	4893	QY	5914	CACAAGAAGATAGAGTAGTATTTTGAATTTGTATTTTCGGTCTGCTTACTGGACTTCT	5973
Db	3937	TCAAGAGCTGATGGGTGCCAGTGTGTGAGGAGAAACCATCCATTTATGGTGCAGCAATT	3996	Db	5017	CACAAGAAGATAGAGTAGTATTTTGAATTTGTATTTTCGGTCTGCTTACTGGACTTCT	5076
QY	4894	TGCATTAAGAAATATGATGACAAAGAAATTTTCCTTTTCAAGAAAAGTAAAGAAAGTGG	4953	QY	5974	TTCTTTTTCACCTTAATTTTAACTTTGGTTTAAAGCTTTTATTTGGAATGCTTAACCTGGA	6033
Db	3997	TGCATTAAGAAATATGATGACAAAGAAATTTTCCTTTTCAAGAAAAGTAAAGAAAGTGG	4056	Db	5077	TTCTTTTTCACCTTAATTTTAACTTTGGTTTAAAGCTTTTATTTGGAATGCTTAACCTGGA	5136
QY	4954	CAACTAAATACATCTCTTTCTGTGTGAAAAGGAGAGATCTTAGGACTATTTGGGTCCAA	5013	QY	6034	GAACCAAGAAGCAGCATTTGAAATTTTCTAAGCTCCCTTAATTTGAAATGCTGTGTTGTTG	6093
Db	4057	CAACTAAATACATCTCTTTCTGTGTGAAAAGGAGAGATCTTAGGACTATTTGGGTCCAA	4116	Db	5137	GAACCAAGAAGCAGCATTTGAAATTTTCTAAGCTCCCTTAATTTGAAATGCTGTGTTGTTG	5196
QY	5014	ATGGTCTGGCAAAAGCACAATTTATTAATTTCTGGTTGGTGATATTGAACCAACTTCAG	5073	QY	6094	TTTTGCTTTTCTTTAAATAAAGCTATGTATATAATTAAGTGAAGCTGCATGTTGTAATGA	6153
Db	4117	ATGGTCTGGCAAAAGCACAATTTATTAATTTCTGGTTGGTGATATTGAACCAACTTCAG	4176	Db	5197	TTTTGCTTTTCTTTAAATAAAGCTATGTATATAATTAAGTGAAGCTGCATGTTGTAATGA	5256
QY	5074	GCCAGTATTTTATGAGATATTCTTTCAGACACAGTGAAGATGATGATTCACCTGAAGT	5133	QY	6154	AGTATATTGAACATATATAGTTTGTATGTCATCTTTTTCACCAATTCAGAAACAGTCTTCT	6213
Db	4177	GCCAGTATTTTATGAGATATTCTTTCAGACACAGTGAAGATGATGATTCACCTGAAGT	4236	Db	5257	AGTATATTGAACATATATAGTTTGTATGTCATCTTTTTCACCAATTCAGAAACAGTCTTCT	5316
QY	5134	GTATGGGTTACTGTCTCAGATAAAACCCCTTTGTGGCCAGATACTACATTCGAGGAACATT	5193	QY	6214	GAATTTGTGATTTTAAAGGAATTGTATAAGTAAGTTTATTTTAAAGTTATCTTTAAGTT	6273
Db	4237	GTATGGGTTACTGTCTCAGATAAAACCCCTTTGTGGCCAGATACTACATTCGAGGAACATT	4296	Db	5317	GAATTTGTGATTTTAAAGGAATTGTATAAGTAAGTTTATTTTAAAGTTATCTTTAAGTT	5376
QY	5194	TTGAATTTATGAGAGCTGTCAAGGAATGAGTGCAGTGAAGTGAAGTGAAGTCAATAGTC	5253	QY	6274	TATGCCATCTCTTTAATAAAGTACGTAATGTTCCATCTTAATAAATAAATAAATAAATAA	6333
Db	4297	TTGAATTTATGAGAGCTGTCAAGGAATGAGTGCAGTGAAGTGAAGTGAAGTCAATAGTC	4356	Db	5377	TATGCCATCTCTTTAATAAAGTACGTAATGTTCCATCTTAATAAATAAATAAATAAATAA	5436
QY	5254	GAATAACACATGCACTTTGATTTTAAAGAAACATCTTTCAGAAAGTCTTAAAGAAACAT	5313	QY	6334	CTAATGCATAGAAAAGATACATAAAGCAATGTGAAAAGTT	6372
Db	4357	GAATAACACATGCACTTTGATTTTAAAGAAACATCTTTCAGAAAGTCTTAAAGAAACAT	4416	Db	5437	CTAATGCATAGAAAAGATACATAAAGCAATGTGAAAAGTT	5475
QY	5314	CAGGAATCAAAACGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCTCAGATTAATT	5373	RESULT 6			
Db	4417	CAGGAATCAAAACGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCTCAGATTAATT	4476	ABS57749			
QY	5374	TGCTAGATGAACCATCTACAGTATGGATCCCAAGCCAAACAGCACATGTGGCAGCAA	5433	ID	ABS57749	standard; cDNA; 5463 BP.	
Db	4477	TGCTAGATGAACCATCTACAGTATGGATCCCAAGCCAAACAGCACATGTGGCAGCAA	4536	XX	ABS57749;		
QY	5434	TTCGAACTGCATTTAAAAACAGAAAGCGGCTGTCTTCTGACCACTCACTATATGGAGG	5493	AC	ABS57749;		
Db	4537	TTCGAACTGCATTTAAAAACAGAAAGCGGCTGTCTTCTGACCACTCACTATATGGAGG	4596	XX	04-FEB-2003 (first entry)		
QY	5494	AGCAGAGCTGTCTGTGATCGAGTACGTATCATGTGTCTGGGAGGTAGATGATTCG	5553	XX	cDNA encoding novel human ATP binding cassette ABCA5 transporter #1.		
Db	4597	AGCAGAGCTGTCTGTGATCGAGTACGTATCATGTGTCTGGGAGGTAGATGATTCG	4656	XX	Human; ATP binding cassette; ABC; ABCA5; transporter;		
QY	5554	GAACAGTCAACATCTAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTAATTTGA	5613	XX	neurotoxin transport; beta-amyloid peptide; chromosome mapping;		
Db	4657	GAACAGTCAACATCTAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTAATTTGA	4716	XX	blood brain barrier transport; tissue typing; predictive medicine;		
QY	5614	AGACTGTGATAGAAAACCTTAGAAGTAGACCGCTTCAAGAGAAATTCAGTATATTTTCC	5673	XX	ABCA5 mediated disorder; ABCA5 related disorder; gene therapy; gene; ss.		
Db	4717	AGACTGTGATAGAAAACCTTAGAAGTAGACCGCTTCAAGAGAAATTCAGTATATTTTCC	4776	OS	Homo sapiens.		
QY	5674	CAATGCAAGCGTCAGGAAGTTTCTCTCTATTTTGGCTTATATAAATTCCTAAGGAAG	5733	XX	Key	Location/Qualifiers	
Db	4777	CAATGCAAGCGTCAGGAAGTTTCTCTCTATTTTGGCTTATATAAATTCCTAAGGAAG	4836	PH	114.5030	/tag=	
QY	5734	ATGTTTCAGTCCCTTTTACAAATCTTTTAAAGCTGGAAGAGCTAAACATGCTTTGCCA	5793	FT	114.5030	/product= "ABCA5"	
Db	4837	ATGTTTCAGTCCCTTTTACAAATCTTTTAAAGCTGGAAGAGCTAAACATGCTTTGCCA	4896	FT		/note= "ATP binding cassette (ABC) A5 transporter"	
QY	5794	TTGAGAAATATAGCTTTTCTCAGCAACATTCGACAGGTTTTCGTAGAACTCACTAAG	5853	XX		/transl_except= (pos:3273..3275, aa:Ser)	
Db	4897	TTGAGAAATATAGCTTTTCTCAGCAACATTCGACAGGTTTTCGTAGAACTCACTAAG	4956	PN	US2002123107-A1.		
				XX	05-SEP-2002.		
				XX	01-MAR-2002; 2002US-00090458.		
				XX	02-MAR-2001; 2001US-0272885P.		
				XX	(ACTI-) ACTIVE PASS PHARM INC.		
				XX	Chen H, Kilinski L, Le Bihan S;		
				XX			

DR WPI: 2003-066798/06.
XX P-PSDB; ABG72423.
PT Novel isolated ATP binding cassette transporter family polypeptide,
PT ABCA5, useful for treating disorders associated with aberrant or unwanted
XX ABCA5 transporter expression or activity.
PS Claim 2; Fig 1; 52pp; English.
XX
CC The invention describes an isolated ATP binding cassette (ABC)
CC transporter family polypeptide (I), designated ABCA5. (I) or the
CC polynucleotide encoding it (II) are useful as targets for developing
CC modulating agents to regulate a variety of cellular processes,
CC particularly the transport of neurotoxic molecules, e.g., beta-amyloid
CC peptide (Abeta), across cell membranes or, e.g., the blood brain barrier
CC (BBB), as targets for developing modulating agents of multi-drug
CC resistance, as diagnostic and therapeutic tools, or to treat disorders
CC associated with aberrant or unwanted ABCA5 transporter expression or
CC activity. (I), (II) or a host cell (III) expressing (II) are useful in
CC screening assays, detection assays (e.g., chromosomal mapping, tissue
CC typing, forensic biology), predictive medicine (e.g., diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenomics), and
CC in methods of treatment (e.g., therapeutic and prophylactic). (I) or
CC (III) are useful as reagents or targets in assays applicable to treatment
CC and diagnosis of ABCA5-mediated or related disorders. (I) is useful to
CC screen for naturally occurring ABCA5 substrates; to screen for drugs or
CC compounds which modulate ABCA5 activity; as a bait protein in a yeast two
CC -hybrid or three-hybrid assay; and to identify other proteins which bind
CC to or interact with ABCA5. (II) is useful in: gene therapy; to detect
CC ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5
CC activity; to locate gene regions associated with genetic disease or to
CC associate ABCA5 with the disease, to identify an individual from a minute
CC biological sample (tissue typing), and to aid in forensic identification
CC of the biological sample. This sequence encodes a novel human ATP binding
CC cassette (ABC) A5 transporter
XX
SQ Sequence 5463 BP; 1699 A; 912 C; 1055 G; 1794 T; 0 U; 3 Other;
Query Match 80.5%; Score 5255.8; DB 10; Length 5463;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 5340; Conservative 0; Mismatches 8; Indels 50; Gaps 3;
QY 994 AGGTTTATTCAGAAACATGCTCCACTGCAATAGGAGGTAGGAGTTGGAGACAGACCA 1053
DB 97 AGGTTTATTCAGAAACATGCTCCACTGCAATAGGAGGTAGGAGTTGGAGACAGACCA 156
QY 1054 GAACACTTCTACTGAAGAAATTAATTAATGAGAAACCAAAAGAGTAGTGTTCAGG 1113
DB 157 GAACACTTCTACTGAAGAAATTAATTAATGAGAAACCAAAAGAGTAGTGTTCAGG 216
QY 1114 AAATCTTTTCCACTATTTTATTTTGGTTAAATTAATTAATGAGAAACCAAAAGAGTAGTGTTCAGG 1173
DB 217 AAATCTTTTCCACTATTTTATTTTGGTTAAATTAATTAATGAGAAACCAAAAGAGTAGTGTTCAGG 276
QY 1174 ATAAGAAATATGAAGAGTGCCTAATATAGAACTCAATCCCTATGGACAAGTTTACTCTTT 1233
DB 277 ATAAGAAATATGAAGAGTGCCTAATATAGAACTCAATCCCTATGGACAAGTTTACTCTTT 336
QY 1234 CTAACTAATCTTGGATATCTCCAGTGCATTAATTAATTAATGAGAAACCAAAAGAGTAGTGTTCAGG 1293
DB 337 CTAACTAATCTTGGATATCTCCAGTGCATTAATTAATTAATGAGAAACCAAAAGAGTAGTGTTCAGG 396
QY 1294 TGTCTACTGATCATCTACTGTATGTCATAATTAATTAATGAGAAACCAAAAGAGTAGTGTTCAGG 1353
DB 397 TGTCTACTGATCATCTACTGTATGTCATAATTAATTAATGAGAAACCAAAAGAGTAGTGTTCAGG 456
QY 1354 TGTTAACATCCAGTCTCTTAAGCCGAGCAACTTTGATGAGTGTGGTTTCAAAGACTTCCA 1413
DB 457 TGTTAACATCCAGTCTCTTAAGCCGAGCAACTTTGATGAGTGTGGTTTCAAAGACTTCCA 516
QY 1414 TGTCTACTGATCATCTACTGTATGTCATAATTAATTAATGAGAAACCAAAAGAGTAGTGTTCAGG 1473
DB 517 TGTCTACTGATCATCTACTGTATGTCATAATTAATTAATGAGAAACCAAAAGAGTAGTGTTCAGG 1536
QY 1474 CAAGAGCTGGCTGTTTCAAAATCATGTGAGGCTGCTCAGTACTGCTCCTCAGGTTTCACAG 1533
DB 577 CAAGAGCTGGCTGTTTCAAAATCATGTGAGGCTGCTCAGTACTGCTCCTCAGGTTTCACAG 636
QY 1534 TTTTCAAGCATCCATAGANGCTCCCATATATACAGTTTGAAGACCAATGTTTCTTTGGGA 1593
DB 637 TTTTCAAGCATCCATAGATGCTGCCATTATACAGTTTGAAGACCAATGTTTCTTTGGGA 696
QY 1594 AGGAGCTGGAGTCAACTAAAGCTGTTTATGGGAGAAACCTGCTGTTGTAGAAATAGATA 1653
DB 697 AGGAGCTGGAGTCAACTAAAGCTGTTTATGGGAGAAACCTGCTGTTGTAGAAATAGATA 756
QY 1654 CTTTCCCGGAGGAGTAATTTAATATACCTAGTTATAGCAATTTTACCTTTTGGTACT 1713
DB 757 CTTTCCCGGAGGAGTAATTTAATATACCTAGTTATAGCAATTTTACCTTTTGGTACT 816
QY 1714 TTTTGGCAATTCATATCGTACAGAAAGAAATAAAAGAAATTTTAAAGATAA 1773
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QY 1774 TGGGACTTCATGACTGCTCTTTTGGCTTTTCTGGGTTCTTCTATATACAAAGTTAATTT 1833
DB 877 TGGGACTTCATGACTGCTCTTTTGGCTTTTCTGGGTTCTTCTATATACAAAGTTAATTT 936
QY 1834 TTCCTATGCTCTCTTATGCGAGTCATGCGAGCTTCTTGTATTTTCTCCTCAAGTA 1893
DB 937 TTCCTATGCTCTCTTATGCGAGTCATGCGAGCTTCTTGTATTTTCTCCTCAAGTA 996
QY 1894 GCAGCAATTTGATATTTCTGTTTTTTCCTTTTATGATTTATCATCTGTATTTTGTCTT 1953
DB 997 GCAGCAATTTGATATTTCTGTTTTTCTTTTATGATTTATCATCTGTATTTTGTCTT 1056
QY 1954 TAATGCTGACACCTCTTTTAAAGAAATCAAAACATGCGGAATAGTGAATTTTGTGTA 2013
DB 1057 TAATGCTGACACCTCTTTTAAAGAAATCAAAACATGCGGAATAGTGAATTTTGTGTA 1116
QY 2014 CTGTGGCTTTTGGATTTATTTGGCTTTATGATAATTCCTCATAGAAAGTTTCCCAATPCGT 2073
DB 1117 CTGTGGCTTTTGGATTTATTTGGCTTTATGATAATTCCTCATAGAAAGTTTCCCAATPCGT 1176
QY 2074 TAGTGGCTTTTTCAGTCTCTTCTGTCACCTGTTTGTGATTTTGTGATTTGTCACAGTCA 2133
DB 1177 TAGTGGCTTTTTCAGTCTCTTCTGTCACCTGTTTGTGATTTTGTGATTTGTCACAGTCA 1236
QY 2134 TGCAATTTAGAAAGATTTTAAAGAGTGTCTTCAATTTTCAAAATTTGACTGCGAGGCCATATC 2193
DB 1237 TGCAATTTAGAAAGATTTTAAAGAGTGTCTTCAATTTTCAAAATTTGACTGCGAGGCCATATC 1296
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4815 AAGCTGAAAGACTAAGAGCTCAAGAGCTGATGGGTGCGAGTGTGTGAGGAGAAACA 4874
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5115 GATGATGATTCACCTGAAGTGTATGGGTACTGCTCCTCAGATAAACCCCTTTGTGGCCAGAT 5174
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5175 ACTACATGAGGAACAATTTTGAATTTATGGAGCTGTCAAGGATGATGTCAGAGTAC 5234
4266 ACTACATGAGGAACAATTTTGAATTTATGGAGCTGTCAAGGATGATGTCAGAGTAC 4325
5235 ATGAAAGAGTCATAAGTCGAATTAACAACATGCACTTGATTTAAAGAAACATCTTCAGAAG 5294
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4686 TTTTGGAAATTAATTAAGAGCTGATGATGAGAAACCTAGAGTAGACCGCTTCAAGA 4745
5655 GAAATTCAGTATATTTTCCCAATGCAAGCGGTGAGGAAAGTTTCTTCTATTTGGCT 5714
4746 GAAATTCAGTATATTTTCCCAATGCAAGCGGTGAGGAAAGTTTCTTCTATTTGGCT 4805
5715 TATAAAATTCCTAAGAAAGATGTTCCAGTCCCTTTTCAAAATCTTTTAAAGCTGAGAA 5774
4806 TATAAAATTCCTAAGAAAGATGTTCCAGTCCCTTTTCAAAATCTTTTAAAGCTGAGAA 4865
5775 GCTAAACATGCTTTTGGCAATTCAGAAATATAGCTTTTCTCAGCAACATTCGAAAGCTT 5834
4866 GCTAAACATGCTTTTGGCAATTCAGAAATATAGCTTTTCTCAGCAACATTCGAAAGCTT 4925

5835 TTTGTAGAACTCACTAAGAAACAAGAGGAGAAATAATAGTTGTGGAACTTTTAAACAGC 5894
4926 TTTGTAGAACTCACTAAGAAACAAGAGGAGAAATAATAGTTGTGGAACTTTTAAACAGC 4985
5895 ACATTTTGGTGGGAAACGAAACACAAAGAGATAGTAGTATTTTGAATTTGTATGTTTCGG 5954
4986 ACATTTTGGTGGGAAACGAAACACAAAGAGATAGTAGTATTTTGAATTTGTATGTTTCGG 5045
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5046 TCTGCTTACTGGGACTTCTTTCTTTTCACTTAATTTTAACTTTGGTTTAAAGAGTTT 5105
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5166 GAAATGCTGTGGTGTGTTTCTTTTCTTTAAATTAAGAGTATGATATAATTAAGTGA 5225
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5226 AGCTGCATGTTTGTATGAAAGTATATTGAACATATATAGTTTGTATGTCATCTTTTCAAC 5285
6195 ATTCAAGAAACAGTCTTCTGAAATTTGTGATTTTAAAGGAATTTGTAATAGAATAGTTTATT 6254
5286 ATTCAAGAAACAGTCTTCTGAAATTTGTGATTTTAAAGGAATTTGTAATAGAATAGTTTATT 5345
6255 TTTAAGTTATCTTTAAGTTTATGCACTTCTTTTAAATTAAGTACGTAATGTTCCCAATCTAA 6314
5346 TTTAAGTTATCTTTAAGTTTATGCACTTCTTTTAAATTAAGTACGTAATGTTCCCAATCTAA 5405
6315 ATAAAGAACTAATACATACTAATGATAGAAAGATACATAAGAAAGTATGTAAGATTT 6372
5406 ATAAAGAACTAATCTAATACTAATGATAGAAAGATACATAAGAAAGTATGTAAGATTT 5463

RESULT 7
AAD37620
ID AAD37620 standard; cDNA; 5262 BP.

XX AAD37620;
XX AC AC
XX DT DT
XX DE DE
XX DE Human transporter protein cDNA #3.
XX KW Human; novel human protein; NHP; transporter protein; mental disorder;
XX KW cancer; gene therapy; drug screening; nutraceutical application;
XX KW cosmetic application; polymorphism; ss.
XX OS Homo sapiens.
XX XX
XX PN WO200231147-A2.
XX XX
XX PD 18-APR-2002.
XX XX
XX PF 04-OCT-2001; 2001WO-US031113.
XX XX
XX PR 10-OCT-2000; 2000US-0239629P.
XX XX
XX XX (LEXI-) LEXICON GENETICS INC.
XX XX Hu Y, Nepomnichy B;
XX XX WPI; 2002-454552/48.
XX XX
XX XX Novel nucleic acid molecule encoding novel human proteins, useful for
XX XX therapeutic, diagnostic and pharmacogenomic applications.
XX PS Disclosure; Page 45-46; 46pp; English.
XX XX

CC The present sequence is a cDNA coding for novel human protein (NHP),
CC human transporter protein. NHPs shares structural similarity with the
CC mammalian ATP-binding cassette (ABC) transporters and multidrug
CC resistance transporters. NHP polynucleotides are useful for the
CC therapeutic, diagnostic and pharmacogenomic applications. They are used
CC for detecting and treating mental disorders and cancers. They are also
CC used in gene therapy. NHP polypeptides are useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of diseases and
CC disorders, and cosmetic or nutraceutical applications
XX
SQ Sequence 5262 BP; 1615 A; 888 C; 1012 G; 1743 T; 0 U; 4 Other;

Query Match 80.4%; Score 5247.4; DB 6; Length 5262;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 5248; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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Db 1 ACTGTTGATATGGTGGTATTTCAAATTCGTGCTACCTATTTACATGCGCTTGTACT 60

QY 817 TTTCAGAGCTGACAGATTCCTGCTCCTCATGATCTGTCAGTTTCCTAAGAGACAGCT 876
Db 61 TTTCAGAGCTGACAGATTCCTGCTCCTCATGATCTGTCAGTTTCCTAAGAGACAGCT 120

QY 877 TGGAGTATCTTAATCCATCTTACCTGGGACGAAACAGCTGCTTATTTGCGGTTAAA 936
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QY 937 ATTACATGAGTTTACTGCGTGGCTCCGGTTTGTGTTGTTTCTCTTTAATAGG 996
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QY 997 TTTATTCGAAACATGTCCTCAATTCAGGAGGTAGGAGTTGGAGACAGACCAGAA 1056
Db 241 TTTATTCGAAACATGTCCTCAATTCAGGAGGTAGGAGTTGGAGACAGACCAGAA 300

QY 1057 CACTTCTACTGAAGAACTACTTAAATGAGAGACCAAAAGAGTAGTGTTCAGGAAA 1116
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QY 1117 TTCTTTTCCACTATTTTATTTGTTTAAATTAATTAATAGCATGATGATCAATA 1176
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QY 1237 ATCTAAATCTTGGATATCTCCAGTGACTATATTTACAGAGCATCATGAGAAAGTGT 1296
Db 481 ATCTAAATCTTGGATATCTCCAGTGACTATATTTACAGAGCATCATGAGAAAGTGT 540

QY 1297 CTACTGATCATCTACCTGATGTCATAATCTAGAGATATACAAATGAGAAAGAAATGT 1356
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QY 1477 GAGCTGGTGTTCAAAATCATGTCAGGCTGCTCAGTACTGCTCCTCAGGTTTTCACAGTTT 1536
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DB 5221 TTTTTCACCTAAATTTTAACTTTGGTTTAAAAAGTTTTT 5258
RESULT 8
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ID AAD37618 standard; cDNA; 4929 BP.
XX
AC AAD37618;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human transporter protein cDNA #1.
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KW Human; novel human protein; NHP; transporter protein; mental disorder;
KW cancer; gene therapy; drug screening; nutraceutical application; gene;
KW cosmetic application; polymorphism; ss.
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FH Key Location/Qualifiers
CDS 1..4929
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FT FT /note= "This degenerate base represents a polymorphic
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FT FT misc_feature 2494
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FT FT site"
FT FT misc_feature 2878
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FT FT site"
XX WO200231147-A2.
XX
XX 18-APR-2002.
XX
XX 04-OCT-2001; 2001WO-US031113.
XX
XX 10-OCT-2000; 2000US-0239629P.
XX (LEXI-) LEXICON GENETICS INC.
XX Hu Y, Nepomnuchy B;
XX
XX WPI: 2002-454552/48.
XX P-PSDB; AAE23656.
XX
XX Novel nucleic acid molecule encoding novel human proteins, useful for
XX therapeutic, diagnostic and pharmacogenomic applications.
XX Claim 1; Page 34-35; 46pp; English.
XX
XX The present sequence is a cDNA coding for novel human protein (NHP),
XX human transporter protein. NHPs shares structural similarity with the
XX mammalian ATP-binding cassette (ABC) transporters and multidrug
XX resistance transporters. NHP polynucleotides are useful for the
XX therapeutic, diagnostic and pharmacogenomic applications. They are used
XX for detecting and treating mental disorders and cancers. They are also
XX used in gene therapy. NHP polypeptides are useful for diagnosis, drug
XX screening, clinical trial monitoring, treatment of diseases and
XX disorders, and cosmetic or nutraceutical applications
XX
XX Sequence 4929 BP; 1544 A; 827 C; 950 G; 1604 T; 0 U; 4 Other;
XX
Query Match 75.4%; Score 4918.4; DB 6; Length 4929;
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Best Local Similarity 99.8%; Pred. No. 0;			
Matches 4919; Conservative 4; Mismatches 6; Indels 0; Gaps 0;			
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QY	1071	AATTAATTAATTAATGACAGACCAAAAGAGTAGTGTTCAGGAATTTCTTTTCCACTA	1130
DB	61	AATTAATTAATTAATGACAGACCAAAAGAGTAGTGTTCAGGAATTTCTTTTCCACTA	120
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QY	1191	GTGCTTAATATAGACTCAATCCTATGACAGAGTTTACTCTTCTTAATCTAAATCTTTGGA	1250
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QY	1251	TATACTCCAGTCACTAATATTAACAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA	1310
DB	241	TATACTCCAGTCACTAATATTAACAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA	300
QY	1311	CCTGATGTCAATTAATTAACAGAAATATCAAAATGAAAAGAAATGTTAAACATCCAGTCTC	1370
DB	301	CCTGATGTCAATTAATTAACAGAAATATCAAAATGAAAAGAAATGTTAAACATCCAGTCTC	360
QY	1371	TCTAAGCCGAGCAACTTTGTAGGTGTGTTTCAAAGACTCCATGTCTTAATGAATCTCGT	1430
DB	361	TCTAAGCCGAGCAACTTTGTAGGTGTGTTTCAAAGACTCCATGTCTTAATGAATCTCGT	420
QY	1431	TTTTTTTCCGTGATGATCCAGTACTCTCTATTTATATATGGAATCAAGAGCTGGCTGTTC	1490
DB	421	TTTTTTTCCGTGATGATCCAGTACTCTCTATTTATATGGAATCAAGAGCTGGCTGTTC	480
QY	1491	AAATCATGTAGAGCTGCTCAGTACTGTGCTCAGGTTTCA CAGTTTCAAGCAATCCATA	1550
DB	481	AAATCATGTAGAGCTGCTCAGTACTGTGCTCAGGTTTCA CAGTTTCAAGCAATCCATA	540
QY	1551	GATGCTGCCATTAATACAGTTGAAGACCAATGTTCTCTTGGAGGAGCTGGAGTCAACT	1610
DB	541	GATGCTGCCATTAATACAGTTGAAGACCAATGTTCTCTTGGAGGAGCTGGAGTCAACT	600
QY	1611	AAAGCTGTTATATGGGAGAACTGCTGTTGTAGAAATAGATATACCTTTCCCGAGGAGTA	1670
DB	601	AAAGCTGTTATATGGGAGAACTGCTGTTGTAGAAATAGATATACCTTTCCCGAGGAGTA	660
QY	1671	ATTTTAAATATACCTAGTTATAGCATTTTCACTTTTGGATATCTTTTGGCAATTCATATC	1730
DB	661	ATTTTAAATATACCTAGTTATAGCATTTTCACTTTTGGATATCTTTTGGCAATTCATATC	720
QY	1731	GTAGCGAAAAAGAAAAATTAAGAAATTTTAAAGATAATGGGACTTCATGATACT	1790
DB	721	GTAGCGAAAAAGAAAAATTAAGAAATTTTAAAGATAATGGGACTTCATGATACT	780
QY	1791	GCCTTTTGGCTTTCTCGGGTCTCTATATACAGTTTAAATTTTCTTATGCTCCCTCTT	1850
DB	781	GCCTTTTGGCTTTCTCGGGTCTCTATATACAGTTTAAATTTTCTTATGCTCCCTCTT	840
QY	1851	ATGGCAGTCAATTCGACAGCTCTTTGTATTTCTCTAAAGTAGCAGCATTTGTGATTTT	1910
DB	841	ATGGCAGTCAATTCGACAGCTCTTTGTATTTCTCTAAAGTAGCAGCATTTGTGATTTT	900
QY	1911	CTGCTTTTCTCTTTATGGATTAATCATCTGTATTTTGTGTTTAAATGCTGACACCTCTT	1970
DB	901	CTGCTTTTCTCTTTATGGATTAATCATCTGTATTTTGTGTTTAAATGCTGACACCTCTT	960
QY	1971	TTTTAAAAATCAAAACATGTGGGAATGTGGAATTTTGTGTTTGTACTGTGGCTTTTGATTT	2030
DB	961	TTTTAAAAATCAAAACATGTGGGAATGTGGAATTTTGTGTTTGTACTGTGGCTTTTGATTT	1020
QY	2031	ATTGGCTTTATGATAATCCTCATAGAAAGTTTTCCTCAAAATCGTTAGTGTGGCTTTTCAGT	2090

3171 GAACTCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTAACAAGAAAT 3230
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2161 GAATCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTAACAAGAAAT 2220
QY |||||
3231 GACCAACAATCTGTGTATAGCTTGCCTTTCAAGGACATGGAACAAATTTTCAGGTTTGTTT 3290
Db |||||
2221 GACCAACAATCTGTGTATAGCTTGCCTTTCAAGGACATGGAACAAATTTTCAGGTTTGTTT 2280
QY |||||
3291 TCTGCCCTTAGACAGCTCAATTCAAATTTGGGGTGTCAATTTCTTATGGTGTTCATGACGACT 3350
Db |||||
2281 TCTGCCCTTAGACAGCTCAATTCAAATTTGGGGTGTCAATTTCTTATGGGTTTCCATGACGACT 2340
QY |||||
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QY |||||
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Db |||||
2401 GTATTTTACTCAGCAGCCACTGGAGGAGAAATGGATTCAAAATCTTTTATGAGAAATGAA 2460
QY |||||
3471 CAGAGCTTACTTATCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGG 3530
Db |||||
2461 CAGAGCTTACTTATCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGG 2520
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3531 AAACAACAGATGTATACATAGCAAGTTTCATTTCTTTACCTTGAACGTTGAAGTAA 3590
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2521 AAACAACAGATGTATACATAGCAAGTTTCATTTCTTTACCTTGAACGTTGAAGTAA 2580
QY |||||
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Db |||||
2581 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTT 2640
QY |||||
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Db |||||
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QY |||||
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Db |||||
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QY |||||
3771 GCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAGCAGAAACATAATGGTGACG 3830
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3831 ATGATTATAGCAGTGACTATGATCTCGTGGCTCCCATAGTGCGGCTTAAATGTGATG 3890
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QY |||||
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QY |||||
4311 AAGTTCCTCTGCTGCTGTTTTTGGCTTATTTGGTATTTTCCATCAGTTATTTCTGTTCACT 4370
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3361 TATATTGCTTCTTCTTCACTTTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCAATTTATC 3420
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Db |||||
3781 AATGAGATGAAGATGAAGATGTCAAGCTGAAAGATCAAGCTCAAGAGCTGATGGGT 3840
QY |||||
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4911 GACAAGAAAGATTTTCTTCTTCAAGAAAGTAAAGAAAGTGGCAACTTAAATATACATCTCT 4970
Db |||||
3901 GACAAGAAAGATTTTCTTCTTCAAGAAAGTAAAGAAAGTGGCAACTTAAATATACATCTCT 3960
QY |||||
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Db |||||
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4201 GTCAAGGAAATGAGTCAAGTCAATGAAAGAAATTTAAAGTCAATTAACATCACTCACTT 4260
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Db |||||
4261 GATTTHAAAGACATCTTTCAGAAAGCTGTAAAGAAATTTACTCTGAGGAAATCAAGCAAG 4320
QY |||||
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Db 4321 TTGTGTTTTCCTCTAAGTATGCTAGGAAATCCTCAGATTACTTTGCTAGATGAACCATCT 4380
QY 5391 ACAGGTATGATCCCAAGACCAACACAGCACATGTGGGAGCAATTCGAATCTGATTTAAA 5450
Db 4381 ACAGGTATGATCCCAAGACCAACACAGCACATGTGGGAGCAATTCGAATCTGATTTAAA 4440
QY 5451 AACAGAAAGCGGCTGCTATTCTGACCACTCACTATATGGAGGAGGAGGCTGTCTGT 5510
Db 4441 AACAGAAAGCGGCTGCTATTCTGACCACTCACTATATGGAGGAGGAGGCTGTCTGT 4500
QY 5511 GATCAGTAGCTATCATGTGCTGGGAGTTAAGATGTATCGGAAACAGTACACATCTA 5570
Db 4501 GATCAGTAGCTATCATGTGCTGGGAGTTAAGATGTATCGGAAACAGTACACATCTA 4560
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Db 4561 AAGAGTAAATTTGGAAGGCTACTTTTGGAAATTAATTTGAAGGACTGGATAGAAAAC 4620
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Db 4621 CTAGAAGTAGCCGCTTCAAGAGAAATTCAGTATATTTTCCCAATGCAAGCCGTCAG 4680
QY 5691 GAAAGTTTCTCTATTTCCTGCTATATAAATTCCTAAGGAAGTGTTCAGTCCCTTCA 5750
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QY 5811 TCTCAAGCAACATTTGGAAACAGGTTTTTGTAGAACTCACTAAGAAACAGAGGAGAGAT 5870
Db 4801 TCTCAAGCAACATTTGGAAACAGGTTTTTGTAGAACTCACTAAGAAACAGAGGAGAGAT 4860
QY 5871 ATAGTTGGAACCTTAAACAGCACACTTTTGGGGAACCAACACAGAGATAGATGA 5930
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QY 5931 GTATTTTGA 5939
Db 4921 GTATTTTGA 4929
```

RESULT 9

ABS57750
ID ABS57750 standard; cDNA; 4917 BP.

XX AC ABS57750;

XX DT 04-FEB-2003 (first entry)

XX DE Coding sequence of human ATP binding cassette ABCA5 transporter #1.

XX KW Human; ATP binding cassette; ABC; ABCA5; transporter;

XX KW neurotoxin transport; beta-amyloid peptide; chromosome mapping;

XX KW blood brain barrier transport; tissue typing; predictive medicine;

XX KW ABCA5 mediated disorder; ABCA5 related disorder; gene therapy; gene; ss.

XX OS Homo sapiens.

XX FH Key

XX CDS Location/Qualifiers

FT 1..4917

FT /*tag= a

FT /product= "ABCA5"

FT /note= "ATP binding cassette (ABC) A5 transporter"

FT /transl_except= (pos:3160..3162, aa:ser)

XX PN US2002123107-A1.

XX PD 05-SEP-2002.

XX XX 01-MAR-2002; 2002US-00050458.

XX PF

XX 02-MAR-2001; 2001US-0272885P.
XX (ACTI-) ACTIVE PASS PHARM INC.
XX PI Chen H, Kilinski L, Le Bihan S;
XX WPI; 2003-066798/06.
XX DR P-PSDB; ABG72423.

XX Novel isolated ATP binding cassette transporter family polypeptide, ABCA5, useful for treating disorders associated with aberrant or unwanted ABCA5 transporter expression or activity.

XX Claim 2; Fig 1; 52pp; English.

XX The invention describes an isolated ATP binding cassette (ABC) transporter family polypeptide (I), designated ABCA5. (I) or the polynucleotide encoding it (II) are useful as targets for developing modulating agents to regulate a variety of cellular processes, particularly the transport of neurotoxic molecules, e.g., beta-amyloid peptide (Abeta), across cell membranes or, e.g., the blood brain barrier (BBB), as targets for developing modulating agents of multi-drug resistance, as diagnostic and therapeutic tools, or to treat disorders associated with aberrant or unwanted ABCA5 transporter expression or activity. (I), (II) or a host cell (III) expressing (II) are useful in screening assays, detection assays (e.g., chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics), and in methods of treatment (e.g., therapeutic and prophylactic). (I) or (III) are useful as reagents or targets in assays applicable to treatment and diagnosis of ABCA5-mediated or related disorders. (I) is useful to screen for naturally occurring ABCA5 substrates; to screen for drugs or compounds which modulate ABCA5 activity; as a bait protein in a yeast two-hybrid or three-hybrid assay; and to identify other proteins which bind to or interact with ABCA5. (II) is useful in: gene therapy, to detect ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5 activity; to locate gene regions associated with genetic disease or to associate ABCA5 with the disease, to identify an individual from a minute biological sample (tissue typing), and to aid in forensic identification of the biological sample. This sequence encodes a novel human ATP binding cassette (ABC) A5 transporter

XX SQ Sequence 4917 BP; 1540 A; 821 C; 955 G; 1599 T; 0 U; 2 Other;

Query Match 73.7%; Score 4807.4; DB 10; Length 4917;
Best Local Similarity 98.8%; Pred. No. 0;

Matches 4891; Conservative 0; Mismatches 7; Indels 50; Gaps 3;

QY 1011 ATGTCCTGCAATTAGGAGGTAGGAGTTGGAGACAGACACACCTTCTACTGAAG 1070
Db 1 ATGTCCTGCAATTAGGAGGTAGGAGTTGGAGACAGACACACCTTCTACTGAAG 60

QY 1071 AATTACTTTAATTAATGCAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 1130
Db 61 AATTACTTTAATTAATGCAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 120

QY 1131 TTTTCTTTTATTTTGGTTAATTAATTAATGATGATGATCCCAATTAAGAAATGAAGAA 1190
Db 121 TTTTCTTTTATTTTGGTTAATTAATTAATGATGATGATCCCAATTAAGAAATGAAGAA 180

QY 1191 GTGCCCTAATAGAACTCAATCTCTATGGCAAGTTTACTCTTTCTAATCTAATCTTTGGA 1250
Db 181 GTGCCCTAATAGAACTCAATCTCTATGGCAAGTTTACTCTTTCTAATCTAATCTTTGGA 240

QY 1251 TATCTCCAGTGACTAATATATACAGCAGGATCATGCGAAGAGTGCTACTGATCATCTA 1310
Db 241 TATCTCCAGTGACTAATATATACAGCAGGATCATGCGAAGAGTGCTACTGATCATCTA 300

QY 1311 CCGTATGTCATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1370
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Qy	1371	TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTCAAAGACTCCATGTCTCTATGAACCTTCGT	14350
Db	361	TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTCAAAGACTCCATGTCTCTATGAACCTTCGT	420
Qy	1431	TTTTTTCCTGATATGATCCAGTATCTCTATATTTATATGGATTCAAAGAGCTGGCTGTTC	1490
Db	421	TTTTTTCCTGATATGATTCAGTATCTCTATATTTATATGGATTCAAAGAGCTGGCTGTTC	480
Qy	1491	AAATCATGTGAGGTGCTCAGTACTGTPCCTCAGTTTTCACAGTTTTCACAGCATCCATA	1550
Db	481	AAATCATGTGAGGTGCTCAGTACTGTPCCTCAGTTTTCACAGTTTTCACAGCATCCATA	540
Qy	1551	GATGCTGCCATTATACAGTTCGAAGCAACGTTCTCTTTCTGGAGGAGCTGGAGTCAACT	1610
Db	541	GATGCTGCCATTATACAGTTCGAAGCAACGTTCTCTTTCTGGAGGAGCTGGAGTCAACT	600
Qy	1611	AAAGCTGTTATTATGGGAGAAACTGCTGTGTGTAGAAATAGATACCTTTCCCGAGGAGTA	1670
Db	601	AAAGCTGTTATTATGGGAGAAACTGCTGTGTGTAGAAATAGATACCTTTCCCGAGGAGTA	660
Qy	1671	ATTTTAAATATACCTAGTTTATAGCATTTTACCTTTTGGATACCTTTTGGCAATTCATATC	1730
Db	661	ATTTTAAATATACCTAGTTTATAGCATTTTACCTTTTGGATACCTTTTGGCAATTCATATC	720
Qy	1731	GTAGCAGAAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACT	1790
Db	721	GTAGCAGAAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACT	780
Qy	1791	GCCTTTTGGCTTTCTCGTGGTTCCTCTATATACAAAGTTTAAATTTTCTTATGTCCCTCTTT	1850
Db	781	GCCTTTTGGCTTTCTCGTGGTTCCTCTATATACAAAGTTTAAATTTTCTTATGTCCCTCTTT	840
Qy	1851	ATGGCAGTCATTGGCAGACGCTTCTTTGTTATTTCTCTCAAAGTACAGCATTTGTCATATTT	1910
Db	841	ATGGCAGTCATTGGCAGACGCTTCTTTGTTATTTCTCTCAAAGTACAGCATTTGTCATATTT	900
Qy	1911	CTGCTTTTTCCTTTATGGATTATCATCTGTATTTTTTGGTTTAAATGCTGACACCTCTTT	1970
Db	901	CTGCTTTTTCCTTTATGGATTATCATCTGTATTTTTTGGTTTAAATGCTGACACCTCTTT	960
Qy	1971	TTTAAABAAATCAAACATGTCGGAAATAGTTCGAAATTTTGTACTGTGGCTTTTGGATTT	2030
Db	961	TTTAAABAAATCAAACATGTCGGAAATAGTTCGAAATTTTGTACTGTGGCTTTTGGATTT	1020
Qy	2031	ATTGGCCTTTATGATAATCCTCATAGAAAGTTTTCCCAAATCGTTAGTGTGGCTTTTCAGT	2090
Db	1021	ATTGGCCTTTATGATAATCCTCATAGAAAGTTTTCCCAAATCGTTAGTGTGGCTTTTCAGT	1080
Qy	2091	CCTTTCTGCTACTGTACTTTTGTGATTTGGAATTCGACAGGTCATGCAATTTTAGAAGATTTT	2150
Db	1081	CCTTTCTGCTACTGTACTTTTGTGATTTGGAATTCGACAGGTCATGCAATTTTAGAAGATTTT	1140
Qy	2151	AATGAAGTGTCTTCATTTTCAAATTTGACTCGAGGCCCATCTCTCTAAATATTACAATTT	2210
Db	1141	AATGAAGTGTCTTCATTTTCAAATTTGACTCGAGGCCCATCTCTCTAAATATTACAATTT	1200
Qy	2211	ATCATGCTCACATTTAATAGTATATCTATGTCTCTTTGGCTGTCTATCTGTGATCAAGTC	2270
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Qy	2271	ATTCAGGGGAATTTGGCTTACGAGATCATCTTTATATTTTCTGTGAGCCTTCATATTTG	2330
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Qy	2331	TCAAAGAGTAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT	2390
Db	1321	TCAAAGAGTAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT	1380
Qy	2391	TTTATGTGAATATTATGACCGAGTTTCTTCAGAAATTTGTAGAAAGAGCCATAGAAATT	2450
Db	1381	TTTATGTGAATATTATGACCGAGTTTCTTCAGAAATTTGTAGAAAGAGCCATAGAAATT	1440
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4352 ATCAGTTATTTGATCAATATTTGCTTCTTCCACTTTTAAGAAATTTTAAATACCA 4411
3330 ATCAGTTATTTGATCAATATTTGCTTCTTCCACTTTTAAGAAATTTTAAATACCA 3389
4412 AGAATTTTGGTCAATTTATCTATCTGCGGAGCTTGNCTTGTATTGCAATCACTGAAT 4471
3390 AGAATTTTGGTCAATTTATCTATCTGCGGAGCTTGGCTTGTATTGCAATCACTGAAT 3449
4472 AACTTTCTTTTGGGATACAAATTTGCAACTATTTCTTCAATATGCTTTTGTATCATCAT 4531
3450 AACTTTCTTTTGGGATACAAATTTGCAACTATTTCTTCAATATGCTTTTGTATCATCAT 3509
4532 TCCAAATCTATCAATCTTAGGTTGCTGATTTCTTTCAAGATTTCTTGGAGATGTT 4591
3510 TCCAAATCTATCAATCTTAGGTTGCTGATTTCTTTCAAGATTTCTTGGAGATGTT 3569
4592 ACGAAAAATGAGACCTTATATCCATGGATAGGCTTTTTCAGTAGCTGTTATATGCC 4651
3570 ACGAAAAATGAGACCTTATATCCATGGATAGGCTTTTTCAGTAGCTGTTATATGCC 3629

4652 TTACTCTCAGTGTGTACTGTGGATTTTCTCTTACANTACTATCAGAAAAAATATCGAGG 4711
3630 TTACTCTCAGTGTGTACTGTGGATTTTCTCTTACANTACTATCAGAAAAAATATCGAGG 3689
4712 CAGATCAATTAAGAAAAAGATCCCTTTTTCAGAAAACTTTTCAACGAAGTCTAAAAATAGAA 4771
3690 CAGATCAATTAAGAAAAAGATCCCTTTTTCAGAAAACTTTTCAACGAAGTCTAAAAATAGAA 3749
4772 GCTTCCGAACCCACGACCAATGAGGATGAAGATGAAGATGTCGAAGCTCAAAAGCTAAA 4831
3750 GCTTCCGAACCCACGACCAATGAGGATGAAGATGAAGATGTCGAAGCTCAAAAGCTAAA 3809
4832 GGTCAAAAGAGCTGATGGTTGCCAGTGTGTGAGGAGAAAACCCATCCATTTATGTTGTCAGCA 4891
3810 GGTCAAAAGAGCTGATGGTTGCCAGTGTGTGAGGAGAAAACCCATCCATTTATGTTGTCAGCA 3869
4892 TTTGCATAAAGATATATGATGACAAAGAAAGATTTTCTCTTTCAGAAAAAGTAAAGAAAGT 4951
3870 TTTGCATAAAGATATATGATGACAAAGAAAGATTTTCTCTTTCAGAAAAAGTAAAGAAAGT 3929
4952 GGCAACTTAATACATCTCTTCTCTGTCGAAAAAGGAGAGATCTTAGGACTTATTTGGGTCC 5011
3930 GGCAACTTAATACATCTCTTCTCTGTCGAAAAAGGAGAGATCTTAGGACTTATTTGGGTCC 3989
5012 AAATGCTGCTGCAAAAGCACAAATTTAATATTCTGTTGTTGATATTGAACCAACTTC 5071
3990 AAATGCTGCTGCAAAAGCACAAATTTAATATTCTGTTGTTGATATTGAACCAACTTC 4049
5072 AGGCCAGGATTTTATGAGATATTCTTTCAGAGACCAAGTGAAGATGATGATTCACCTGAA 5131
4050 AGGCCAGGATTTTATGAGATATTCTTTCAGAGACCAAGTGAAGATGATGATTCACCTGAA 4109
5132 GTGTATGGTTTACTGCTCTCAGATAAAACCCCTTTGTGGCCAGATCTACATTTGCAGGAACA 5191
4110 GTGTATGGTTTACTGCTCTCAGATAAAACCCCTTTGTGGCCAGATCTACATTTGCAGGAACA 4169
5192 TTTTGAAATTTATGAGCTGTCAAAGGAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5251
4170 TTTTGAAATTTATGAGCTGTCAAAGGAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4229
5252 TCGAATAACACATGCACTTGAATTTAAAGAACATCTTTCAGAGACCTGTAAAGAAACTACC 5311
4230 TCGAATAACACATGCACTTGAATTTAAAGAACATCTTTCAGAGACCTGTAAAGAAACTACC 4289
5312 TCGAGGAATCAAAACGAAAGTTGCTGTTTCTTAAAGTATGCTAGGGAATCTCAGATTAC 5371
4290 TCGAGGAATCAAAACGAAAGTTGCTGTTTCTTAAAGTATGCTAGGGAATCTCAGATTAC 4349
5372 TTTGCTAGATGAACCATCTACAGGTATGGATCCCAAGCCAAACAGCACATGTGGGAGC 5431
4350 TTTGCTAGATGAACCATCTACAGGTATGGATCCCAAGCCAAACAGCACATGTGGGAGC 4409
5432 AATTCGAATGCAATTTTAAACAGAAAGCGGCTGCTATTCTGACCACTCCTCATATATGGA 5491
4410 AATTCGAATGCAATTTTAAACAGAAAGCGGCTGCTATTCTGACCACTCCTCATATATGGA 4469
5492 GGAGGAGAGGCTGTGCTGTGATGAGTACTATCATGTTGCTGTTGGCAGTTAAGATGAT 5551
4470 GGAGGAGAGGCTGTGCTGTGATGAGTACTATCATGTTGCTGTTGGCAGTTAAGATGAT 4529
5552 CGGAAACAGTACACATCTTAAAGATTAATTTGCGAAAGGCTACTTTTGGAAATTTAAAT 5611
4530 CGGAAACAGTACACATCTTAAAGATTAATTTGCGAAAGGCTACTTTTGGAAATTTAAAT 4589
5612 GAAGGACTGGATAGAAAACTTGAAGTAGACCGCTTCAAGAGAAATTCAGTATATTTT 5671
4590 GAAGGACTGGATAGAAAACTTGAAGTAGACCGCTTCAAGAGAAATTCAGTATATTTT 4649
5672 CCCAAATGCAAGCCGTGAGAAAGTTTCTTCTTATTTTGGCTTATAAATTCCTTAAGGA 5731
4650 CCCAAATGCAAGCCGTGAGAAAGTTTCTTCTTATTTTGGCTTATAAATTCCTTAAGGA 4709

3719	QY	ACCTGGAGACAAACCACATAAATACAAAAAAGCTCTGCTTCTTCAAATTTCTGCT-----	3777
721	Db	ACCTGGAGACAAACCACATAAATACAAAAAAGCTCTGCTTCTTCAAATTTCTGCTGTGA	780
3774	QY	-----GACTCAGATATCAGTGCATCTTATTAGCTTTTTCACAAGCCAGCAACATAA	3822
781	Db	GAGTGTGTGAAGACTTCAGATATCTGTGATCTTATTAGCTTTTTCACAAGCCAGCAACATAA	840
3823	QY	TGCTGACGATGATTAAATGACAGTGACTATGATCCGTGGCTGCCCATAGTGGCGCTTTAA	3882
841	Db	TGGTGACGATGATTAAATGACAGTGACTATGATCCGTGGCTGCCCATAGTGGCGCTTTAA	900
3883	QY	ATGTGATGCATTACAGAAAAAGCATATGTTTTTGCAGCTGTGTTTTCAACAGTACTATGGTTT	3942
901	Db	ATGTGATGCATTACAGAAAAAGCATATGTTTTTGCAGCTGTGTTTTCAACAGTACTATGGTTT	960
3943	QY	ATTTCTTTACCTATATTAGTGAATATCATTAGTAAGTAACTACTCTTTATCATTTAAATGTGA	4002
961	Db	ATTTCTTTACCTATATTAGTGAATATCATTAGTAAGTAACTACTCTTTATCATTTAAATGTGA	1020
4003	QY	CTGAAACCATCCAGATCTGGAGTACCCCATTTCTTCAAGAAATPACTGATATAGTTTTTA	4062
1021	Db	CTGAAACCATCCAGATCTGGAGTACCCCATTTCTTCAAGAAATPACTGATATAGTTTTTA	1080
4063	QY	AAATGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTTACTGCAATGCCACTT	4122
1081	Db	AAATGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTTACTGCAATGCCACTT	1140
4123	QY	ACTTTGCCATGAAAAATGCAGAGATCATAGATCAAAAGCTTATACTCAACTTAAACTTTT	4182
1141	Db	ACTTTGCCATGAAAAATGCAGAGATCATATA-----	1170
4183	QY	CAGTCTTTTGGCAATCGCATATTTGGATTTGGACAAGCTGTGTTGTGATATCCCTTATTTT	4242
1171	Db	-AGTCTTTTGGCAATCGCATATTTGGATTTGGACAAGCTGTGTTGTGATATCCCTTATTTT	1222
4243	QY	TTATCATTCTTTATTTTGTATGCTAGGAAGCTTACTGGCAATTTCAATTATGGAATATATTTT	4302
1230	Db	TTATCATTCTTTATTTTGTATGCTAGGAAGCTTACTGGCAATTTCAATTATGGAATATATTTT	1282
4303	QY	ATACTGAAAGTTCCTTGCTGTGTTTTTTCCTTATTTGGTTATGTTCCTACAGTTATTC	4362
1290	Db	ATACTGAAAGTTCCTTGCTGTGTTTTTTCCTTATTTGGTTATGTTCCTACAGTTATTC	1342
4363	QY	TGTTCACTATATTGCTTCTTTACCTTTAAGAAAAATTTTAAATACCAAGAAATTTTCGT	4422
1350	Db	TGTTCACTATATTGCTTCTTTACCTTTAAGAAAAATTTTAAATACCAAGAAATTTTCGT	1402
4423	QY	CATTATATCTATTCTGTGGCAGCTGTCGTTATTTGCAATCACTGAAATAACTTTCTTTTA	4482
1410	Db	CATTATATCTATTCTGTGGCAGCTGTCGTTATTTGCAATCACTGAAATAACTTTCTTTTA	1462
4483	QY	TGGGATACACAATTGCCAATCTCTTCATATTATGCTTTTGTATCATTCATCCAACTATTC	4542
1470	Db	TGGGATACACAATTGCCAATCTCTTCATATTATGCTTTTGTATCATTCATCCAACTATTC	1522
4543	QY	CACTTCTAGGTGCTGATTTCTTTTATAGAAATTTCTTGAAGAAATGCTACGAAAAAATG	4602
1530	Db	CACTTCTAGGTGCTGATTTCTTTTATAGAAATTTCTTGAAGAAATGCTACGAAAAAATG	1582
4603	QY	TGGACACCTATAAATCCATGGGATAGGCTTTTCAGTAGCTGTTTATATCGCTTACCTGCAGT	4662
1590	Db	TGGACACCTATAAATCCATGGGATAGGCTTTTCAGTAGCTGTTTATATCGCTTACCTGCAGT	1642
4663	QY	GTGTACTGTGGATTTTTCCTCTTACAATACTAGAAAAAATATCGAGCGCATCAATAA	4722
1650	Db	GTGTACTGTGGATTTTTCCTCTTACAATACTAGAAAAAATATCGAGCGCATCAATAA	1702
4723	QY	GAAAAAGATCCCTTTTTCAGAAACCTTTCAAACGAAGTCTAAAAATAGGAAGCTTCCAGAAC	4782
1710	Db	GAAAAAGATCCCTTTTTCAGAAACCTTTCAAACGAAGTCTAAAAATAGGAAGCTTCCAGAAC	1762

4783 CACCAGCAATGAGATGAAGATGTCACAAAGCTGAAGACTAAAGGTCAAGAGC 4842
1770 CACCAGCAATGAGATGAAGATGTCACAAAGCTGAAGACTAAAGGTCAAGAGC 1829
4843 TGATGGTGGCAGTGTGTGAGGAGAAACCAATCATTTATGGTCAGCAATTTGCATAAAG 4902
1830 TGATGGTGGCAGTGTGTGAGGAGAAACCAATCATTTATGGTCAGCAATTTGCATAAAG 1889
4903 AATATGATGACAGAAAGATTTTCTCTTCAAGAAAGATGAAGAAAGTGGCACTAAAT 4962
1890 AATATGATGACAGAAAGATTTTCTCTTCAAGAAAGATGAAGAAAGTGGCACTAAAT 1949
4963 ACATCTCTTTCTGTGTGAGAAAGAGAGATCTTAGGACTATTTGGGTCCAAATGGTGTG 5022
1950 ACATCTCTTTCTGTGTGAGAAAGAGAGATCTTAGGACTATTTGGGTCCAAATGGTGTG 2009
5023 GCAAAAGCAATTAATTAATTTCTGTGTGAGATTAATGAACCACTTCAGGCCAGGTAT 5082
2010 GCAAAAGCAATTAATTAATTTCTGTGTGAGATTAATGAACCACTTCAGGCCAGGTAT 2069
5083 TTTTAGGAGATTAATTTCTCAGAGACAAGTGAAGATGATGATTCAGTGAAGTGTATGGTT 5142
2070 TTTTAGGAGATTAATTTCTCAGAGACAAGTGAAGATGATGATTCAGTGAAGTGTATGGTT 2129
5143 ACTGCTCTCAGATAAACCCCTTTGTGGCCAGATACATACATTCAGGAAATTTTGAATTT 5202
2130 ACTGCTCTCAGATAAACCCCTTTGTGGCCAGATACATACATTCAGGAAATTTTGAATTT 2189
5203 ATGGAGCTGTCAAGGAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5262
2190 ATGGAGCTGTCAAGGAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2249
5263 ATGCACTTGAATTTAAAGAACTCTTCAGAGACTGTAAAGAACTACCTCAGGAATCA 5322
2250 ATGCACTTGAATTTAAAGAACTCTTCAGAGACTGTAAAGAACTACCTCAGGAATCA 2309
5323 AACGAAGTGTGTTTGTCTTAAGTATGCTAGGAACTCCTCAGATTAATTTGTAGATG 5382
2310 AACGAAGTGTGTTTGTCTTAAGTATGCTAGGAACTCCTCAGATTAATTTGTAGATG 2369
5383 AACCACTACAGATGATGATCCCAAGCAACAGACACATGTGGCAGCAATTCGAACCTG 5442
2370 AACCACTACAGATGATGATCCCAAGCAACAGACACATGTGGCAGCAATTCGAACCTG 2429
5443 CATTTAAACAGAAAGCGGGTGTCTATCTGACCACTCATATATGAGGAGGAGGAGG 5502
2430 CATTTAAACAGAAAGCGGGTGTCTATCTGACCACTCATATATGAGGAGGAGGAGG 2489
5503 CTGCTCTGATCGAGTAGCTATCATGTTCTGCGCAGTGAAGATGATCGGAACAGTAC 5562
2490 CTGCTCTGATCGAGTAGCTATCATGTTCTGCGCAGTGAAGATGATCGGAACAGTAC 2549
5563 AACATCTAAAGATTAATTTGAAAGGCTACTTTTGGAAATTAATTTGAAGGACTGGA 5622
2550 AACATCTAAAGATTAATTTGAAAGGCTACTTTTGGAAATTAATTTGAAGGACTGGA 2609
5623 TAGAAAACCTAGAGTAGCCCTTCAAGAGAAATTCAGTATATTTTCCCAATGCAA 5682
2610 TAGAAAACCTAGAGTAGCCCTTCAAGAGAAATTCAGTATATTTTCCCAATGCAA 2669
5683 GCCGTGAGAAAGTGTCTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGT 5742
2670 GCCGTGAGAAAGTGTCTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGT 2729
5743 CCCTTTCACATCTTTTATAGCTGGAAGAGCTAAACATGCTTTTCCATTTGAAGAT 5802
2730 CCCTTTCACATCTTTTATAGCTGGAAGAGCTAAACATGCTTTTCCATTTGAAGAT 2789
5803 ATAGCTTTTCTCAAGCAATTTGGAACAGAGTGTGTTAGAACTCCTAAGAAACAGAGG 5862
2790 ATAGCTTTTCTCAAGCAATTTGGAACAGAGTGTGTTAGAACTCCTAAGAAACAGAGG 2849
5863 AGGAAGATTAATGTTGTGGAACCTTTAAACAGACACACTTTGTTGGGAACCAACAGAG 5922

2850 AGGAAGATTAATGTTGTGGAACCTTTAAACAGACACACTTTGGTGGGAACCAACAGAAG 2909
5923 ATAGAGTAGTATTTGAAATTTGTAATTTGTTGGTCTGCTTACTGGGACTTCTTTCTTTTC 5982
2910 ATAGAGTAGTATTTGAAATTTGTAATTTGTTGGTCTGCTTACTGGGACTTCTTTCTTTTC 2969
5983 ACTTAATTTTAACTTTTGGTTTAAAGATTTTATTTGGAATGTAATCTGAGAACCAAGA 6042
2970 ACTTAATTTTAACTTTTGGTTTAAAGATTTTATTTGGAATGTAATCTGAGAACCAAGA 3029
6043 ACCGACTGGAATTTTCTTAAAGCTCCTTAATTTGAAATGCTGCTGTTGTTGCTTT 6102
3030 ACCGACTGGAATTTTCTTAAAGCTCCTTAATTTGAAATGCTGCTGTTGTTGCTTT 3089
6103 TCTTTAAATAAAACGATGATATAATTAAGTGAAGCTGCATGTTTGTATTGAAGTATATTG 6162
3090 TCTTTAAATAAAACGATGATATAATTAAGTGAAGCTGCATGTTTGTATTGAAGTATATTG 3149
6163 AACTATATAGTTTGTATGTCATCTTTTCCATTCCAGAAACAGTCTTCTGAATTTGTG 6222
3150 AACTATATAGTTTGTATGTCATCTTTTCCATTCCAGAAACAGTCTTCTGAATTTGTG 3209
6223 ATTTAAGGAATTTGTAATGATGATGTTTATTTTAAAGTATCTTTAAAGTTTATGCCATC 6282
3210 ATTTAAGGAATTTGTAATGATGATGTTTATTTTAAAGTATCTTTAAAGTTTATGCCATC 3269
6283 TTTCTTAAATAAGTACGTAATGTTTCCAACTTAAATAAAACCTAATACTAATAATGCAAT 6342
3270 TTTCTTAAATAAGTACGTAATGTTTCCAACTTAAATAAAACCTAATACTAATAATGCAAT 3329
6343 AGAAAAGATACATAAAGC 6360
3330 AGAAAAGATACATAAAGC 3347

RESULT 12

ADAS3416

ID ADAS3416 standard; cDNA; 3268 BP.

XX AC ADAS3416;

XX AC AC

DT 20-NOV-2003 (first entry)

XX Human coding sequence, SEQ ID 984.

DE Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;

XX Gene Therapy; human; secretory protein; membrane proteins; cancer;

KW inflammatory disease; osteoporosis; neurological disease; gene; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Naganari K, Masuho Y;

XX WPI; 2003-395539/38.
DR P-PSDB; ADA55055.
XX New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in

PT which the gene is involved, or as target molecules for gene therapy.
XX
PS Claim 1; SEQ ID NO 984; 205pp; English.
XX The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
XX inflammatory diseases, osteoporosis or neurological disease.
SQ Sequence 3268 BP; 1022 A; 540 C; 622 G; 1084 T; 0 U; 0 Other;
Query Match 48.7%; Score 3178; DB 10; Length 3268;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 3224; Conservative 0; Mismatches 6; Indels 33; Gaps 1;
3102 ATGTTCTCTCAAAAGTAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATAT 3161
Db 6 ATGTTCTCTCAAAAGTAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATAT 65
3162 TGTGCGACAGATCTCTTCTCACTGGTTAAACACATATACCTGGAGCTACTTTATTA 3221
Db TGTGCGACAGATCTCTTCTCACTGGTTAAACACATATACCTGGAGCTACTTTATTA 125
3222 CAACAGATGACCAACAACTTGTGTATAGCTTGCCTTCAAGGACATGGAACAAATTTCA 3281
Db 126 CAACAGATGACCAACAACTTGTGTATAGCTTGCCTTCAAGGACATGGAACAAATTTCA 185
3282 G-----GTTTGTCTTCTGCGCTAGACAGTCAT 3308
Db 186 GGAATGTCTGATAGACAAAAGGATGTTATGTATGTTTCTGCGCTAGACAGTCAT 245
3309 TCAAAATTTGGGTGTCATTTCTTATGTTTCCATGACGACTTTGGAGACGCTATTTTTA 3368
Db 246 TCAAAATTTGGGTGTCATTTCTTATGTTTCCATGACGACTTTGGAGACGCTATTTTTA 305
3369 AGCTTAGAAGTGAAGCAGAAATGACCAACAGATATAGTGTATTTACTCAGCAGCCA 3428
Db 306 AAGCTTAGAAGTGAAGCAGAAATGACCAACAGATATAGTGTATTTACTCAGCAGCCA 365
3429 CTGAGGAGAAATGGATTCAAAATCTTTTATGAAATGGAACAGAGCTTACTTATTCCT 3488
Db 366 CTGAGGAGAAATGGATTCAAAATCTTTTATGAAATGGAACAGAGCTTACTTATTCCT 425
3489 TCTGAAACCAAGGCTTCTAGTGAGCAGCAGTATGAGCTTTGGAAACACAGATGTATACA 3548
Db 426 TCTGAAACCAAGGCTTCTAGTGAGCAGCAGTATGAGCTTTGGAAACACAGATGTATACA 485
3549 ATAGCAAAAGTTTCATTTCTTTACCTTGAACGTCGAAAGTAAATCAGTGAGATCAGTGTG 3608
Db 486 ATAGCAAAAGTTTCATTTCTTTACCTTGAACGTCGAAAGTAAATCAGTGAGATCAGTGTG 545
3609 CTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTGGTTCATCTCTTTT 3668
Db 546 CTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTGGTTCATCTCTTTT 605
3669 AAAAAATGCTGTGTTTCCCATCAAACTTCTTCCAGACTTATATTTTCAAAACCTGGAGAC 3728
Db 606 AAAAAATGCTGTGTTTCCCATCAAACTTCTTCCAGACTTATATTTTCAAAACCTGGAGAC 665
3729 AAACACATATAACAAACAAAGTCTGCTTCTTCAAAATTCGTGTGATCAGTATCAGT 3788
Db 666 AAACACATATAACAAACAAAGTCTGCTTCTTCAAAATTCGTGTGATCAGTATCAGT 725
3789 GATCTTATAGCTTTTTCACAGCCAGAACATATATGTTGAGATGATTAATGACAGTGAC 3848
Db 726 GATCTTATAGCTTTTTCACAGCCAGAACATATATGTTGAGATGATTAATGACAGTGAC 785
3849 TATGATACCGTGGCTCCCAATAGTGGCTTTTAAATGTGATGCAATCAGAAAAAGGACTAT 3908
Db 786 TATGATACCGTGGCTCCCAATAGTGGCTTTTAAATGTGATGCAATCAGAAAAAGGACTAT 845
3909 GTTTTTCAGCTGTTTTCACAGCTATGTTTATTTTCTTTTACCTATATATAGTGAATATC 3968

846 GTTTTTCAGCTGTTTTCACAGCTATGTTTATTTTACCTATATATAGTGAATATC 905
Db
3969 ATTAGTAACCTACTATCTTTTAAATGTGACTGAAACCACTCCAGATCTGGAGTACC 4028
Qy
906 ATTAGTAACCTACTATCTTTTAAATGTGACTGAAACCACTCCAGATCTGGAGTACC 965
Db
4029 CCAATCTTTTCAAGAAATTTACTGATATAGTTTTHAAATTTGAGCTGTATTTTCAAGCAGCT 4088
Qy
966 CCAATCTTTTCAAGAAATTTACTGATATAGTTTTHAAATTTGAGCTGTATTTTCAAGCAGCT 1025
Db
4089 TTGCTTGAATCATTTTACTGCAATGCCACCTTACTTTTCCATGGAATAATGACAGAAAT 4148
Qy
1026 TTGCTTGAATCATTTTACTGCAATGCCACCTTACTTTTCCATGGAATAATGACAGAAAT 1085
Db
4149 CATAAGATCAAGCTTATATCTAACTTAACTTTTCAAGTCTTTTCCATCTGATATTTGG 4208
Qy
1086 CATAAGATCAAGCTTATATCTAACTTAACTTTTCAAGTCTTTTCCATCTGATATTTGG 1145
Db
4209 ATTGACAAAGCTGTTTGTATATCCCTTATTTTATCATCTTATTTTGTGCTAGGA 4268
Qy
1146 ATTGACAAAGCTGTTTGTATATCCCTTATTTTATCATCTTATTTTGTGCTAGGA 1205
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4269 AGCTTACTGGCAATTCATATATGATATATTTTATATCTGTAAGTTCCTTGTGTGTT 4328
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1206 AGCTTACTGGCAATTCATATGATATATTTTATATCTGTAAGTTCCTTGTGTGTT 1265
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1266 TTTTGGCTTATTTGGTATTTCCATCATCTTCTGTTTCACTTATATTTGCTTCTTCAAC 1325
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Qy
1326 TTTTGAAGAAATTTTAAATACCAAGAAATTTTGGTCAATTTATCTTCTGTTGGAGGTTG 1385
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4449 NCTTGTATTTGCAATCACTGAAATTAACCTTTTATTTGGATGATACAAATTTCAATTTCT 4508
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1386 GCTTGTATTTGCAATCACTGAAATTAACCTTTTATTTGGATGATACAAATTTCAATTTCT 1445
Db
4509 CATTTATGCTTTTGTATCATCTTCCAATCTATCTTCTAGTGTGCTGATTTCTTCTTC 4568
Qy
1446 CATTTATGCTTTTGTATCATCTTCCAATCTATCTTCTAGTGTGCTGATTTCTTCTTC 1505
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4569 ATAAAGATTTCTTGGAGAAATGTAGCAAAATTTGGACACCTTATATCTCATGAGTAGG 4628
Qy
1506 ATAAAGATTTCTTGGAGAAATGTAGCAAAATTTGGACACCTTATATCTCATGAGTAGG 1565
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4629 CTTTTCAGTAGCTTTATATGCTTCTTACCTGAGTGTGTACTGTGGATTTTCTTCTTACAA 4688
Qy
1566 CTTTTCAGTAGCTTTATATGCTTCTTACCTGAGTGTGTACTGTGGATTTTCTTCTTACAA 1625
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4689 TACTATGAGAAATATGAGGAGGAGTCAATTAAGAAAGATCCCTTTTTCAGAAACCTTT 4748
Qy
1626 TACTATGAGAAATATGAGGAGGAGTCAATTAAGAAAGATCCCTTTTTCAGAAACCTTT 1685
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1686 TCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCAGACCAATGAGGATGAAGTAA 1745
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4809 GATGTCAAGCTGAAAGCTAAAGCTCAAGAGCTGATGGTTCAGCTGTGTGTGAGGAG 4868
Qy
1746 GATGTCAAGCTGAAAGCTAAAGCTCAAGAGCTGATGGTTCAGCTGTGTGTGAGGAG 1805
Db
4869 AAACCATCATTTATGCTGAGCAATTTTGCATAAAGATATGATGACAAAGAAAGATTTTCTT 4928
Qy
1806 AAACCATCATTTATGCTGAGCAATTTTGCATAAAGATATGATGACAAAGAAAGATTTTCTT 1865
Db
4929 CTTTTCAGAAAGTAAAGAGGAGGCAATTAATATCATCTTCTTGTGTGAAAAAGGA 4988
Qy
1866 CTTTTCAGAAAGTAAAGAGGAGGCAATTAATATCATCTTCTTGTGTGAAAAAGGA 1925
Db
4989 GAGATCTTAGCATTTTGGGTCCCAATGCTGCGCAAAAGCAATTTATATATTTCTG 5048
Qy

CC The present invention describes appropriate expression vectors, specific
CC antibodies as well as sense and antisense oligonucleotides, which can be
CC used to modulate protein activity. These proteins have various and
CC distinct uses for example the TGF beta binding proteins are useful for
CC the treatment and prevention of retinal fibrosis, nephritis and heart
CC related ischaemia; proteins that bind modified LDL can treat
CC hyperlipidaemia, familial hypercholesterolaemia and myocardial infarction
CC ; proteins with ATP-binding transporter activity are useful for treating
CC diabetes mellitus, cystic fibrosis, Dubin-Johnson syndrome and Byler's
CC disease; while those with immunoglobulin-like activity can be used to
CC treat or prevent lupus erythematoses, rheumatoid arthritis and
CC hepatitis. Accordingly, these proteins are described with various
CC activities such as nephrotropic, vasotropic, hepatotropic, anilipapenic,
CC antiinflammatory and immunosuppressive. This polynucleotide is a full
CC length murine cDNA sequence encoding a polypeptide of the invention.
XX
SQ Sequence 3950 BP; 1055 A; 802 C; 863 G; 1230 T; 0 U; 0 Other;

Query Match 45.0%; Score 2934.4; DB 10; Length 3950;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 3247; Conservative 0; Mismatches 522; Indels 0; Gaps 0;

QY	991	AATAGGTTTATTCAGAAACATGCCACTGCAATAGGAGGTAGGAGTTGGAGACAGA	1050
DB	181	AGTAACTGACCTAGAAACATGGCTACTGCAATAGGAGTGGAGTTGGAGACAGA	240
QY	1051	CCAGAACACTTCTACTGAGAAATTAATTAATCGAAGCCAAAGAGTAGTGTTC	1110
DB	241	CCAGAACACTTCTACTGAGAAATTAATTAATCGAAGCTAAAGAGTAGTGTTC	300
QY	1111	AGGAAATCTTTTCCACTATTTTTTTATTTGGTTAATTAATTAGCATGATCATC	1170
DB	301	AGGAAATCTTTTCCCTATTTTTTTATTTGGCTGATATTAGTAGCATGATCATC	360
QY	1171	CAATATAGCAATATGAGAACTGCTTAATATAGCACTCAATCTATGGCAAGTTTACTC	1230
DB	361	CAATATAGCAATATGAGAACTGCTTAATATAGCACTCAATCTATGGCAAGTTTACTC	420
QY	1231	TTTCTPAATCTAATCTTTGGATATCTCCAGTGAATAATTAACAAGCAGCATCATCAGA	1290
DB	421	TTTCCAAAGCTTATCTTGGATATCTCCAGTGAATAATTAACAAGCAGCATCATCAGA	480
QY	1291	AAGTGTCTACTGATCAGTCACTGCTATTAATTAAGTGAATAATTAACAAGTGAATAAG	1350
DB	481	GGGTTTGTACGATCATCTTCCAGGTTATAGTACTGAAGATACGCAATATGAGAAAG	540
QY	1351	AAATGTTAACTCCAGTCTCTAAGCCGAGCAACTTTGTAGTGTGGTTTTCAGAGACT	1410
DB	541	AACGTGTAGCCGCAAGCTTTCTTAAGTCCAGCACTTCGTAGTGTGGTTTTCAGAGACA	600
QY	1411	CCATGCTCTATGAACTCGTTTCTTCTGATGATTCAGTATCTTCTATTTATATGG	1470
DB	601	CCATGCTCTATGAACTCGTTTCTTCTGATGATTCAGTATCTTCTATTTATATGA	660
QY	1471	ATTCAGAGCTGGCTGTTTCAAAATCATGTGAGGCTGCTCAGTACTGCTCAGGTTTCA	1530
DB	661	ATTCAGAGAGGCTGTTTCAAAAGCATGTGATGCTGCTCAGTACTGCTTGGGTTTA	720
QY	1531	CAGTTTACAGGATCCATAGATGCTGCCATATACAGTTGAGACCAATGTTCTCTTT	1590
DB	721	CAGTTTCTCAGGATCCATAGATGCTGCCATATACAGCTGAGACCAATGTTCTGTTG	780
QY	1591	GGAGGAGCTGGAGTCAAACTGATTTATTTGGGAGAAATCTGTTGTTGAGAAATAG	1650
DB	781	GGAGGAGCTGGAGTCCAGCAAACTGTGATCATGGGAGAGCGCGTGTGTGGAGATTG	840
QY	1651	ATACCTTTCCCGGAGGATATTTTATATACCTAGTTATAGCATTTTACCTTTTGGAT	1710
DB	841	ACACCTTCCCGGAGGAGTATCTCATCTACCTCTCATGAGCTTCTCGCCCTTCGGGT	900
QY	1711	ACTTTTGGCAATTCATATCTAGCAGAAAGAAAGAAAGAAATTTTAAAGA	1770
DB	901	ACTTCTGGCAATCCATCTGTCGAGAAAGAAAGAAAGATTTAAAGAAATTTTAAAGA	960

QY	1771	TAATGGGACTTCATGATACCTGCTTTTGGCTTTCTCTGGGTCTTCTATATACAAAGTTAA	1830
DB	961	TAATGGGACTTCATGACACATGCTTTTGGCTTTCTCTGGGTCTTCTATATACAAAGTTAA	1020
QY	1831	TTTTTCTATGCTCCCTCTTCTATGAGCAGTATGCGACAGCTTCTTTGTTATTTCTCAAA	1890
DB	1021	TTTTTCTATGCTCCCTCTTCTATGAGCAGTATGCGACACAGCTTCTTTGTTATTTCTCAAA	1080
QY	1891	GTAGCAGCATGTGATATTTCTGCTTTTCTTTTCTTTATGAGTATCATCTGTATTTTGG	1950
DB	1081	GTAGCAGCATGTGATATTTCTTCTACTGTTCTTTATATGATGTGATCTGTGTTTTTGG	1140
QY	1951	CTTTAATGCTGACACCTCTTTTAAAAAATCAAAAATGAGGAAATAGTTGAATTTTGG	2010
DB	1141	CTTTAATGCTGACACCTCTTTTAAAAAATCAAAAATGAGGAAATAGTTGAATTTTGG	1200
QY	2011	TTACTGTGGCTTTTGGGATTTTATTTGGCTTATGATTAATCTCATAGAAAAGTTTCCCAAT	2070
DB	1201	TCACCGTGGTGTGTTGGATTTTGGCTGCTGATTTCTCTCATAGAAAAGTTTCCCAAGT	1260
QY	2071	CGTTAGTGTGGCTTTTCACTCTTCTGTCATCTGTACTTTTGTGATTTGTTGATTTGACAGG	2130
DB	1261	CGCTGGTGTGGCTTTTCACTCTTCTGTCATCTGTACTTTTGTGATTTGTTGATTTGACAGG	1320
QY	2131	TCATGCAATTTAGAGATTTTAAATGAGGTGCTTCAATTTTCAAAATTTGACTGAGGCGCAT	2190
DB	1321	TCATGCAATTTAGAGATTTTAAAGGGTCCCTTTATTTCTAATTTGACTGAGGTCCCT	1380
QY	2191	ATCCTCTAATTTATPACAAATTTATCATGCTCACATTAATAGTATPATTTCTATGCTCTTGG	2250
DB	1381	ATCCTCTAATTTATPACAAATTTATCATGCTCACATTTGACAGTGTGTTCTATGCTCTCTGG	1440
QY	2251	CTGTCTATCTTGATCAAGTCAATTTCCAGGGAAATTTGGCTTTACGGAGATCATCTTTATTT	2310
DB	1441	CTGTCTATCTTGATCAAGTCAATTTCCAGGGAAATTTGGCTTTACGGAGATCATCTTTATTT	1500
QY	2311	TTCTGAAGCTTCTATTTGCTCAAGAGTAAAGAAATTTATGAGGAGTTATCAGAGGCA	2370
DB	1501	TTTTCAGAGCCATCGTATTTGCTCAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG	1560
QY	2371	ATGTTAATGGAATATTTAGTTTGTGAAATTTATGAGCAGTTTCTTCTCAGAAATTTGTAG	2430
DB	1561	ACATTAATGGCAATTTATGCTCTCAATGAATTTGTTGAGCCGCTTTCTTCTCAGAAATTTATAG	1620
QY	2431	GAAAGAGGCTTATGAGAAATTTAGTGGTATTTCAAGAGACATACAGAAAGAGGGTGAAGATG	2490
DB	1621	GAAAGAGGCTTATGAGAAATTTAGTGGTATTTCAAGAGACATACAGAAAGAGGGTGAAGATG	1680
QY	2491	TGGAGGCTTTTCAAGAAATTTCTCATTTGACATATATGAGGCTCAGATTCTGCTTACTTTG	2550
DB	1681	TGGAGGCTTTTCAAGAAATTTCTCATTTGACATATATGAGGCTCAGATTCTGCTTACTTTG	1740
QY	2551	GCCACAGTGGAAACAGGAAAGAGTACATTTGATGAATATTTCTTGTGAGCTCTGCCACCTT	2610
DB	1741	GCCACAGTGGAAACAGGAAAGAGTACATTTGATGAATATTTCTTGTGAGCTCTGTCTCCACCT	1800
QY	2611	CTGATGGGTTTGCATCTATATATGACACAGTCTCAGAAATAGATGAATGTTTGTAG	2670
DB	1801	CTGATGGGTTTGCATCTATATATGACACAGTCTCAGAAATAGATGAATGTTTGTAG	1860
QY	2671	CAAGAAAAATGATTTGGCATTTGCTCCAGTTCAGATATATAACTTTGTATTTTGTGACAGTAG	2730
DB	1861	CAAGAAAAATGATTTGGCATTTGCTCCAGTTCAGATATATAACTTTGTATTTTGTGACAGTAG	1920
QY	2731	AAGAAAAATTTTCAATTTTGGCTTCAATCAAGGGTATCCAGCCACATATAATATACAG	2790
DB	1921	AAGAAAAATTTTCAATTTTGGCTTCAATCAAGGGTATCCAGCCACATATAATATACAG	1980
QY	2791	AAGTGCAGAAAGTTTCTACTAGATTTTACAGATGAGACTATCAAGATAACCAAGCTTAA	2850
DB	1981	AAGTGCAGAAAGTTTCTACTAGATTTTACAGATGAGACTATCAAGATAACCAAGCTTAA	2040

antilipemic; antiinflammatory; immunosuppressive; LDL.
Mus musculus.
WO2003091435-A1.
06-NOV-2003.
23-APR-2003; 2003WO-JP005174.
23-APR-2002; 2002JP-00120853.
26-APR-2002; 2002JP-00125934.
30-APR-2002; 2002JP-00128505.
02-MAY-2002; 2002JP-00130914.
04-DEC-2002; 2002JP-00352270.
04-DEC-2002; 2002JP-00352619.
04-DEC-2002; 2002JP-00352730.
(RIKE) RIKEN KK.
(DNAP-) DNAFORM KK.
(MITU) MITSUBISHI CHEM CORP.
Hayashizaki Y, Kamiya M, Kubodera H;
WPI; 2003-854404/79.
P-PSDB; ADF74751.
Mouse TGF-beta binding, modified LDL binding, ATP-binding transporter and immunoglobulin-like proteins for screening potential drug substances modifying their activity or expression.
Claim 12; SEQ ID NO 17; 225pp; Japanese.
This invention relates to novel nucleic acids and encoded polypeptides identified in a full-length cDNA library. Specifically, it refers to novel murine proteins (or mutants derived thereof) that either bind to TGF beta family proteins, bind to modified low-density lipoprotein (LDL), exhibit ATP-binding transporter activity or immunoglobulin-like activity. The present invention describes appropriate expression vectors, specific antibodies as well as sense and antisense oligonucleotides, which can be used to modulate protein activity. These proteins have various and distinct uses, for example the TGF beta binding proteins are useful for the treatment and prevention of retinal fibrosis, nephritis and heart related ischaemia; proteins that bind modified LDL can treat hyperlipidaemia, familial hypercholesterolaemia and myocardial infarction; proteins with ATP-binding transporter activity are useful for treating diabetes mellitus, cystic fibrosis, Dubin-Johnson syndrome and Byler's disease; while those with immunoglobulin-like activity can be used to treat or prevent lupus erythematoses, rheumatoid arthritis and hepatitis. Accordingly, these proteins are described with various activities such as nephrotropic, vasotropic, hepatotropic, antilipemic, antiinflammatory and immunosuppressive. This polynucleotide is a full length murine cDNA sequence encoding a polypeptide of the invention.
Sequence 3831 BP; 1021 A; 767 C; 838 G; 1205 T; 0 U; 0 Other;
Query Match 43.0%; Score 2807; DB 10; Length 3831;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 3112; Conservative 0; Mismatches 491; Indels 1; Gaps 1;
991 PATAGTTTATTCAGAAACATGCTCCACTGCAATAGGAGTAGGAGTAGGAGCAGA 1050
227 ATTAACTGACCTGAAACATGGCTACTGCAATAGGAGTAGGAGTAGGAGCAGA 286
1051 CCAGAACACTTCTACTGAAGAACTTACTTAATTAATGAGAACCAAAAGAGTAGTGTTC 1110
287 CCAGAACACTTCTACTGAAGAACTTACTTAATTAATGAGAACCAAAAGAGTAGTGTTC 346
1111 AGGAATCTTTTCCACTATTTTATTTTATTTTGGTGAATTAATTAATGAGTAGTGTTC 1170
347 AGGAATCTTTTCCACTATTTTATTTTATTTTGGTGAATTAATTAATGAGTAGTGTTC 406
1171 CAAATAAGAAATPATGAAGAGTGCCTAATATAGAACTCAATCCTATGAGCAAGTTTACTC 1230

Db 407 CAAATAAGAAATPATGAAGAGTATCTGATATAGAGCTCAGCCCTATGCAAAATTCAGCC 466
Qy 1231 TTTCTAATCTAATTTCTTGGATATATCCAGTGTACTAATATTACAAGCAGCATCATCAGA 1290
Db 467 TTTCCAAAGTTATTTCTTGGATACACTCCCGTGTACTAATATTACAAGCAGCATTCAGCA 526
Qy 1291 AAGTGTCTACTGATCATCTACCTGATGATTAATTAATGAGAAATATACAAATGAAAG 1350
Db 527 GGGTTTCTACCGATCATCTTCCCAAGTTATAGTTACTGAAGATACGCAATGAGAAAG 586
Qy 1351 AAATGTTAAATCCAGTCTCTTAAGCCGAGCAACTTTGAGGTGTGGTTTCCAAAGACT 1410
Db 587 AACTGGTAGCCGAAGTCTTTCTAAGTCCAGCAACTTCGTAGGTGTGGTTTCCAAAGACA 646
Qy 1411 CCATGTCCTATGAACCTTCTTCTCTGATGATGATCCAGTATCTCTATTTATATGG 1470
Db 647 CCATGTCCTATGAACCTTCTTCTCTGATGATGATCCAGTATCTCTATTTATATGA 706
Qy 1471 ATCAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGTCTAGTACTGTCTCAGGTTTCA 1530
Db 707 ATCAAGAGAGAGGCTGTTCAAAAGACATGTGATGCTGTCTAGTACTGTCTTGGGGTTTA 766
Qy 1531 CAGTTTACAGCATCCATAGATGCTGCCAATATACAGTTGAAGACCAATGTTCTCTTT 1590
Db 767 CAGTTTCTGAGGCATCGATAGTCTGCCAATATACAGCTGAAGACCAATGTTCTGTGT 826
Qy 1591 GGAAGGAGCTGGAGTCAACTAAAGCTGTATTATGAGGAGAACTGTCTGTGTGAATAG 1650
Db 827 SGAGCGAGCTGAGTTCGACCAAGCTGTGATCATGCGAGAGGCGCTGTGTGAGATTG 886
Qy 1651 ATACCTTCCCGAGGAGTAATTTTATATATACCTAGTTATAGCATTTTCACTTTTGGAT 1710
Db 887 ACACCTTCCCGAGGAGTCACTCTCATCTACCTGTCTAGTCTTCTCGCCCTTCGGCT 946
Qy 1711 ACTTTTGGCAATCATATCGTAGCAAAAAGAAAAAATAAAGAAATTTTAAAGA 1770
Db 947 ACTTCTGGCAATCCATCTGTGSCAGAAAGAAAGAGTTTAAAGAAATTTTAAAGA 1006
Qy 1771 TAATGGAGCTCATGATGATGCTTTTGGCTTTCTCGGTCTCTTATATACAGTTTAA 1830
Db 1007 TAATGGAGCTCATGATGATGCTTTTGGCTTTCTCGGTCTCTTATATACAGTTTAA 1066
Qy 1831 TTTTCTTATGCTCCCTCTTATGAGCAGTCAATGCGACAGCTTCTTGTATTTCCTCAAA 1890
Db 1067 TTTTCTTATGCTCCCTCTTATGAGTGTGCTGATGCTGCAACAGCTTCTTGTATTCCCTCAGA 1126
Qy 1891 GTAGCAGATTTGATATTTCTGCTTTTCTTTTCTTTATGATATATCATCTGATTTTGG 1950
Db 1127 GTAGCAGATTTGATATTTCTTCTACTGTATTCTTATATGATTTGTCATCTGTGTTTTG 1186
Qy 1951 CTTTAACTGCTCACACCTCTTTTAAATAAATAAAGAAATGAGTAATTTTGAATTTTGG 2010
Db 1187 CTTTAACTGCTCACACCTCTTTTAAATAAATAAAGAAATGAGTAATTTTGAATTTTGG 1246
Qy 2011 TTACTGTGGCTTTTGGATTTATGAGCTTATGATTAATCTCATAGAAAGTTTCCCAAT 2070
Db 1247 TCACCGTGTGTTTGGATTTTGGCTGTGATGTTCTCATAGAAAGTTTCCCAAGGT 1306
Qy 2071 CGTTAGTGTGGCTTTTTCAGTCTCTTCTGTCAGTGTACTTTTGTGATTTGATTTGCAAG 2130
Db 1307 CGTGTGTGGCTCTTTCAGTCTCTTCTGTCAGTGTACTTTTGTGATTTGATTTGCAAG 1366
Qy 2131 TCATGCTATTAAGAGATTTTAAAGAGGTGCTTCATTTTCAAAATTTGACGTGCAAGGCCAT 2190
Db 1367 TCATGCTATTAAGAGATTTTAAAGAGGTGCTTCATTTTCAAAATTTGACGTGCAAGGCCAT 1426
Qy 2191 ATCTCTAATTTATACAAATTTATGCTCACTTATAGTATATTTCTATGCTCTTGG 2250
Db 1427 ATCTCTAATTTATACAAATTTATGCTCACTTATAGTATATTTCTATGCTCTTGG 1486
Qy 2251 CTTGCTATTTCTGATCAAGTCAATTCAGGGAAATTTGGCTTACGGAGATCATCTTTATTT 2310

Db 1487 CTGTGTATCTCGACCAAGTCATCTCCAGGGAAATTTGGCTTGAGGAGGTCACTTTTGTAT 1546
QY 2311 TTCTGAAGCCTTTATATTTGGTC-AAAGAGTAAAGAAATTTATGAGAGTTATCAGAGGC 2369
Db 1547 TTTTGAAGCCATCGTATTTGGTCAAAAACAAAGAACTATAAGGAGTATCGAGGC 1606
QY 2370 AATGTTAATGGAATATTTAGTTTGTAGTGAATATATGAGCAGTTTCTTCGAATTTGTA 2429
Db 1607 AACATTAATGGAATATTTAGTCTCAATGAATTTGTGAGCCGTTTCTTCGAATTTATA 1666
QY 2430 GGAAGAAGAGCCATAAGAAATTTAGTGGTATTCAGAAGACATACAGAAAGAGGGTGAAAT 2489
Db 1667 GGAAGAAGAGCTATAAGAAATTTAGTGGTATTCAGAAATCTTATAGAAAGAACTAGAAC 1726
QY 2490 GTGGAGCCTTTGAGAAATTTGTCTATTTGACATATATGAGGGTCAGATTTACCTTTACT 2549
Db 1727 GTGGAGCCTTTGAGAAATTTGTCTATTTGACATATATGAGGGTCAGATTTACCTTTACT 1786
QY 2550 GGCACAGTGAACAGGAAGAGTACATTTGATGAATATTTCTTTGAGACTCTGCCACCT 2609
Db 1787 GGCACAGTGAACAGGAAGAGTACATTTGATGAATATTTCTTTGAGACTCTGCCACCT 1846
QY 2610 TCTGATGGTTTGCAATTTATATATGACACAGAGTCTCAGAAATAGATGAATTTTGA 2669
Db 1847 TCTGATGGTTTGCAATTTATATATGACACAGAGTCTCAGAAATAGATGAATTTTGA 1906
QY 2670 GCAAGAAATGATTTGCAATTTGTCCTCAAGAGTACAGAGTACAGAGTACAGAGTACAGAGT 2789
Db 1967 GAAAGAAATTTATCAATTTTGGCTTCAATCAAGAGTACAGAGTACAGAGTACAGAGT 2026
QY 2790 GAAAGTGAAGAGTTTTACTAGATTTAGACATGACAGTACAGAGTACAGAGTACAGAGT 2849
Db 2027 GAAAGTGAAGAGTTTTCTGATCTGACATGACAGTACAGAGTACAGAGTACAGAGT 2086
QY 2850 AATTAAGTGGTGGTCAAAAAGAAAGTGTCAATTTAGGAAATTTGCTTTTGGGAAACCA 2909
Db 2087 AATTAAGTGGTGGTCAAAAAGAAAGTGTCTGTAGGAAATTTGCTTTTGGGAAACCA 2146
QY 2910 AATTAAGTGGTGGTCAAAAAGAAAGTGTCTGTAGGAAATTTGCTTTTGGGAAACCA 2969
Db 2147 AATTAAGTGGTGGTCAAAAAGAAAGTGTCTGTAGGAAATTTGCTTTTGGGAAACCA 2206
QY 2970 TGAATCTTTTAAATACAGAAAGCCATCGGGTGAAGGTTTCAAGTGTCTTCAATTTCA 3029
Db 2207 TGAATCTTTTAAATACAGAAAGCCATCGGGTGAAGGTTTCAAGTGTCTTCAATTTCA 2266
QY 3030 GATGAAGTGTCAATTTCTGACATAGGAAAGTGTGTATATCAAGGAAATGCTGAAATGT 3089
Db 2267 GATGAAGTGTCAATTTCTGACATAGGAAAGTGTGTATATCAAGGAAATGCTGAAATGT 2326
QY 3090 GTTGGTCTTTCAATTTCTTCAAGGAAAGTGTGTATATCAAGGAAATGCTGAAATGT 3149
Db 2327 GTTGGTCTTTCAATTTCTTCAAGGAAAGTGTGTATATCAAGGAAATGCTGAAATGT 2386
QY 3150 ATAGACAAATTTGTCACAGAAATCTCTTTCTTCAAGGAAATGCTGAAATGT 3209
Db 2387 ATAGACAAATTTGTCACAGAAATCTCTTTCTTCAAGGAAATGCTGAAATGT 2446
QY 3210 GCTACTTTATACAGAAATGACAAATGCTGTGTATATCAAGGAAATGCTGAAATGT 3269
Db 2447 GCGGCTTACTGACAGAAATGACAAATGCTGTGTATATCAAGGAAATGCTGAAATGT 2506
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Db 2507 GACAAATTTTCAAGGAAATGCTGTGTATATCAAGGAAATGCTGAAATGT 2566
QY 3330 TATGGTGTTCAGAGCTTTTGAAGAGTATTTTGAAGAGTATTTTGAAGAGTATTTTGAAGAG 3389
Db 2567 TATGGTGTTCAGAGCTTTTGAAGAGTATTTTGAAGAGTATTTTGAAGAGTATTTTGAAGAG 2626

QY 3390 ATTGACCAAGCAGATATATAGTGTATTTTACTCAGACGCCACTGGAGGAAAGAAATGATTTCA 3449
Db 2627 ATTGACCAAGCAGATATATAGTGTATTTTACACAGCAGCCGCGGAGGAAAGAAATGATTTCA 2686
QY 3450 AATCTTTTGTGAAATGGAACAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTCTCTA 3509
Db 2687 AATCTTTTGTGAAATGGAACAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTCTCTA 2746
QY 3510 GTGAGCAGATGAGCCTTTGGAAACCAAGAGTATACAAATAGCAAGTTTCAATTTCTTT 3569
Db 2747 GTGAGCAGATGAGCCTTTGGAAACCAAGAGTATACAAATAGCAAGTTTCAATTTCTTT 2806
QY 3570 ACCTTGAAGCGTGAAGTAAATCAGTGAAGTATGAGTGTCTCTCTTTTAAATTTTCTT 3629
Db 2807 TCATTTGAAGCGTGAAGTAAATCAGTGAAGTATGAGTGTCTCTCTTTTAAATTTTCTT 2866
QY 3630 ACAGTTTCAAGTATTTTATTTTGTGTTCTCTCTTTTAAATGCTGTTTCTTCTT 3689
Db 2867 GCAGTTTCAAGTATTTTATTTTCTCTCTCTTTTAAATGCTGTTTCTTCTT 2926
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Db 2927 AAACTTTGTTCCAGACTTATTTTCTTAAACCTGGAGACAAACACATATAAACA 2986
QY 3750 AGTCTGCTTTCTTCAAAATTTCTGCTGACATATCAGTGTATTTTATAGCTTTTCTTCA 3809
Db 2987 AGCTCTGCTTTCTTCAAAATTTCTGCTGACATATCAGTGTATTTTATAGCTTTTCTTCA 3046
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Db 3047 CACCAGAAATATGTTGACGATATTAATGACAGTGTATGATATCGTGGCTTCTTCA 3106
QY 3870 AGTGGGCTTTAAATGTTGATGATTCAGAAAGGACTATGTTTGGAGCTGTTTCAAC 3929
Db 3107 AGTGGGCTTCTCAATGTTGGTGGTCTGAAAGGACTATGTTTGGAGCTGTTTCAAC 3166
QY 3930 AGTACTGTTTATTTCTTTACTATATTTAGTGAATATCATTAGTAACTTACTTCTTAT 3989
Db 3167 AGTACTGTTTATTTGTTTGGCTCATGATGACATCATTTAGTAACTTACTTCTTAT 3226
QY 3990 CATTTAAATGTCATGAAACCATCCAGATCTGAGATCCCATTTCTTCAAGAAATTACT 4049
Db 3227 CATTTAAATGTCATGAAACCATCCAGATCTGAGATCCCATTTCTTCAAGAAATTACT 3286
QY 4050 GATATAGTTTTTAAATGAGCTGATTTTCAAGCAGCTTTTGGTGGATCATTTGTTACT 4109
Db 3287 GACATTTTAAATGAGCTGATTTTCAAGCAGCTTTTGGTGGATCATTTGTTACT 3346
QY 4110 GCAATGCCACCTTACTTTGCCATGGAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAAT 4169
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QY 4170 GCAATTTAACTTTGAGCTTTTGGCTTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 4229
Db 3407 GCAATTTAACTTTGAGCTTTTGGCTTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3466
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Db 3467 ATCCCTTTTATTTTATCATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 3526
QY 4290 GATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 4349
Db 3527 GATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 3586
QY 4350 CCAATGATTTTCTGCTTCACTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 4409
Db 3587 CCAATGATTTTCTGCTTCACTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 3646
QY 4410 AAGAAATTTTGTGCTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 4469
Db 3647 AAGAAATTTTGTGCTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 3706

Db 1201 AACTGCAGTGTGTACTGTGGAATTTCTCTTACAATACTATGAGAAAAATATGAGGCA 1260
Qy 4714 GATCAATAGAAAAGATCCCTTTTTCAGNAAGCTTTCAACGAGTCTAAATAATAGGAGC 4773
Db 1261 GATCAATAGAAAAGATCCCTTTTTCAGNAAGCTTTCAACGAGTCTAAATAATAGGAGC 1320
Qy 4774 TTCCGAACCAACGACAGATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGG 4833
Db 1321 TTCCGAACCAACGACAGATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGG 1380
Qy 4834 TCAAGAGCTGATGGTTCGAGTGTGTGAGGAGAAACCATCCATTATGTGTCAGCAATT 4893
Db 1381 TCAAGAGCTGATGGTTCGAGTGTGTGAGGAGAAACCATCCATTATGTGTCAGCAATT 1440
Qy 4894 TGCATAAAGATATGATGACAAAGAAATTTTCTTCTTCAAGAAAAGTAAAGAAAGTGG 4953
Db 1441 TGCATAAAGATATGATGACAAAGAAATTTTCTTCTTCAAGAAAAGTAAAGAAAGTGG 1500
Qy 4954 CAACTAAATACATCTCTTTCTGTGTAAGAAAAGGAGATCTTAGGACTATTGGGTCGAA 5013
Db 1501 CAACTAAATACATCTCTTTCTGTGTAAGAAAAGGAGATCTTAGGACTATTGGGTCGAA 1560
Qy 5014 ATGGTCTGGCAAGCAATTAATTAATTTCTGTTGGTGATATTCAGCCAACTTCAG 5073
Db 1561 ATGGTCTGGCAAGCAATTAATTAATTTCTGTTGGTGATATTCAGCCAACTTCAG 1620
Qy 5074 GCCAGTATTTTAGGAGATTAATCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAGT 5133
Db 1621 GCCAGTATTTTAGGAGATTAATCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAGT 1680
Qy 5134 GTATGGTTCATCTCTCAGATAAACCCTTTGTGCCAGATACATTCGAGGAACATT 5193
Db 1681 GTATGGTTCATCTCTCAGATAAACCCTTTGTGCCAGATACATTCGAGGAACATT 1740
Qy 5194 TTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAGTGAATGAAGAAAGTCAATAAGTC 5253
Db 1741 TTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAGTGAATGAAGAAAGTCAATAAGTC 1800
Qy 5254 GAATAACACATGACCTTGAATTTAAAGAACATCTTCAGAGACTGTAAAGAACTACCTG 5313
Db 1801 GAATAACACATGACCTTGAATTTAAAGAACATCTTCAGAGACTGTAAAGAACTACCTG 1860
Qy 5314 CAGGAATCAAGCAAGTGTCTTTTGTCTTAAGTATCTAGGGAATCCTCAGATTAATT 5373
Db 1861 CAGGAATCAAGCAAGTGTCTTTTGTCTTAAGTATCTAGGGAATCCTCAGATTAATT 1920
Qy 5374 TCCTAGATGAACCATCTACAGTATGGATCCCAAGCCAAAAGCAGACATGTGGCAGCAA 5433
Db 1921 TCCTAGATGAACCATCTACAGTATGGATCCCAAGCCAAAAGCAGACATGTGGCAGCAA 1980
Qy 5434 TTTCGAACCTGATTTAAAGCAGAGAGGGGTCTTCTGACCACTCAGTATATGGAGG 5493
Db 1981 TTTCGAACCTGATTTAAAGCAGAGAGGGGTCTTCTGACCACTCAGTATATGGAGG 2040
Qy 5494 AGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGCAGTTAAGATGTATCG 5553
Db 2041 AGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGCAGTTAAGATGTATCG 2100
Qy 5554 GAAACAGTCAACATCTAAGAGTAAATTTGAAAGGGCTACTTTTGGAAATTAANTTGA 5613
Db 2101 GAAACAGTCAACATCTAAGAGTAAATTTGAAAGGGCTACTTTTGGAAATTAANTTGA 2160
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Db 2161 AGGACTGGATGAAAACCTAGAGTAGACCGCTTTCAAGAGAAATTCAGTATATTTTCC 2220
Qy 5674 CAAATGCAAGCGTCAAGAAAGTTTCTCTATTTTGGCTTATAAATTCCTAAGGAAG 5733
Db 2221 CAAATGCAAGCGTCAAGAAAGTTTCTCTATTTTGGCTTATAAATTCCTAAGGAAG 2280
Qy 5734 ATGTTTCAGTCCCTTTCACAATCTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCCA 5793
Db 2281 ATGTTTCAGTCCCTTTCACAATCTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCCA 2340

Qy 5794 TTCAAGAAATATAGCTTTTCTCAAGCAACATTGGAACAGGTTTTTGTAGAACTCACTAAAG 5853
Db 2341 TTCAAGAAATATAGCTTTTCTCAAGCAACATTGGAACAGGTTTTTGTAGAACTCACTAAAG 2400
Qy 5854 AACAAAGAGGAGGAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAA 5913
Db 2401 AACAAAGAGGAGGAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAA 2460
Qy 5914 CACAAGAGATAGAGTAGTATTTTGAATTTGTATTTGCTCGGTCTGCTTACTGGACTTCT 5973
Db 2461 CACAAGAGATAGAGTAGTATTTTGAATTTGTATTTGCTCGGTCTGCTTACTGGACTTCT 2520
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Search completed: December 4, 2004, 07:17:06
Job time : 2772 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: December 4, 2004, 06:17:02 ; Search time 18029 Seconds
(without alignments)
13188.155 Million cell updates/sec

Title: US-10-005-338B-1
Perfect score: 6525
Sequence: 1 aaatgttgatattttctct.....ttgatcataataagtgaat 6525

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2934.4	45.0	3950	AK047188	AK047188 Mus muscu
2	2807	43.0	3831	AK046203	AK046203 Mus muscu
3	1209.6	18.5	1529	AK034961	AK034961 Mus muscu
4	1182	18.1	1346	U66672	U66672 Homo sapien
5	978.2	15.0	6017	3 CR627382	CR627382 Homo sapi
6	837	12.8	850	6 CD250953	CD250953 AGENCOURT
7	789.2	12.1	838	6 CD262943	CD262943 AGENCOURT
8	761.4	11.7	872	5 BQ729333	BQ729333 AGENCOURT
9	760.6	11.7	809	3 BC029426	BC029426 Homo sapi
10	751	11.5	4620	9 AY414282	AY414282 Homo sapi
11	741.4	11.4	773	5 BQ441353	BQ441353 AGENCOURT
12	740.2	11.3	874	6 CD629439	CD629439 56046273J
13	736.8	11.3	912	6 CD629443	CD629443 56046401J
14	731	11.2	747	5 BU686259	BU686259 UI-CF-DU1
15	729	11.2	730	6 CR278622	CR278622 TFU00182
16	722.4	11.1	771	4 BG564439	BG564439 602584385
17	722.2	11.1	826	6 CD629435	CD629435 56046257J
18	721	11.0	909	6 CD629437	CD629437 56046265J
19	719.4	11.0	793	6 CR241963	CR241963 UI-CF-FN0
20	706.6	10.8	744	6 CD629440	CD629440 56046281H
21	681.6	10.4	756	4 BG435656	BG435656 602506942
22	680.4	10.4	744	1 AL700140	AL700140 DKZP686H
23	676.4	10.4	697	5 BQ774317	BQ774317 UI-H-B21
24	673.6	10.3	752	5 CD629427	CD629427 55146471J

ALIGNMENTS

RESULT 1
AK047188
LOCUS

DEFINITION

AK047188 3950 bp mRNA linear HTC 03-APR-2004
Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:B93003A02 product:ATP-BINDING CASSETTE
PROTEIN homolog (Homo sapiens), full insert sequence.

ACCESSION AK047188 GI:26338625
VERSION AK047188.1

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

FUBMED

10349636

REFERENCE

AUTHORS

TITLE

JOURNAL

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25	668	10.2	926	5	BU146839
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33	646	9.9	735	4	BG926885
34	643	9.9	663	6	CD629438
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37	633.4	9.7	4594	9	AY414284
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39	631.8	9.7	3890	5	BC053340
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44	623	9.5	623	6	CA773849
45	619.4	9.5	672	6	CD629426

The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,720 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3950)

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FUKUDA,S., FURUNO,M., HANAGAKI,T., HARA,A., HASHIZUME,W.,
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HORI,F., IMOTANI,K., ISHII,Y., ITOH,M., KAGAWA,I., KASUKAWA,T.,
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KOYA,S., KURIHARA,C., MATSUYAMA,T., MIYAZAKI,A., MURATA,M.,
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SOGABE,Y., TAGAMI,M., TAGAWA,A., TAKAHASHI,F., TAKAKU-AKIHARA,S.,
TAKEDA,Y., TANAKA,T., TOMARU,A., TOYA,T., YASUNISHI,A.,
MURAMATSU,M. and HAYASHIZAKI,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>
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ORIGIN

Query Match 45.0%; Score 2934.4; DB 3; Length 3950;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 3247; Conservative 0; Mismatches 522; Indels 0; Gaps 0;

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Qy 1291 AAGTGTCTACTGATCATCTACCTGATGCTAATTAATGAGAAATATACAATGAAAG 1350
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Db 661 ATTCAAGAGAGCTGTTCAAAAGATGATGATGCTGCTCAGTACTGGTCTTGGGGTTA 720
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Db 721 CAGTTCTGAGGATCATGATAGATGCTGCAATATATACATGCTGAAGACCAATGTTCTGTGT 780
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 full-length enriched library, clone B230352G14 product: ATP-BINDING
 CASSETTE PROTEIN homolog [Homo sapiens], full insert sequence.

AK046203
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 HTC; CAP trapper.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
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 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
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 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
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 Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
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 RIKEN integrated sequence analysis (RISA) system-384-format
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 Genome Res. 10 (11), 1757-1771 (2000)
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 The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 695-690 (2001)

5
 The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

6 (bases 1 to 3831)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
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 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.

Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
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RESULT 3
 AK034961
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 AK034961
 VERSION
 AK034961.1 GI:26330331
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus

REFERENCE
 1
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
 2
 Genome Res. 10 (10), 1617-1630 (2000)
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Harada, A., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Okawa, E., Wachi, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 4
 Genome Res. 10 (11), 1757-1771 (2000)
 5
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection Nature 409, 695-690 (2001)

TITLE
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation

JOURNAL REFERENCE AUTHORS	of 60,770 full-length cDNAs		QY	3525	CTTTGGAAACAACAGATGATATACATAGCAAGTTTCATTTCTTACCTTGAACGCGAA	3584
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JOURNAL TITLE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp. URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		QY	3585	AGTAATAACAGTGAGATCAGTGTGCTGCTGCTTTTAAATTTTTCACAGTTCAGATTTT	3644
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://phantom.gsc.riken.jp/ Location/Qualifiers		Db	181	AGCAAAACAGTGGCGCTGTGCTGCTTTTAAATTTTTCAGTTCAGATTTT	240
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	86.9%; Pred No. 1.6e-242; Mismatches 200; Indels 0; Gaps 0;		Db	841	GTGTGTTCTGATTTTGTATGCTAGGAAGCTTACTGGCAATTCATTATGGAATATATTTTAT	900
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RESULT 4
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DEFINITION Homo sapiens clone EST90625 mRNA sequence.
ACCESSION U66672
VERSION U66672.1 GI:1906557
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1346)
AUTHORS Allikmets R., Gerrard, B., Hutchinson, A. and Dean, M.
TITLE Characterization of the human ABC superfamily: isolation and
mapping of 21 new genes using the expressed sequence tags database
JOURNAL Hum. Mol. Genet. 5 (10), 1649-1655 (1996)
MEDLINE 97049974
PUBMED 8894702
REFERENCE 2 (bases 1 to 1346)
AUTHORS Allikmets R., Gerrard, B. and Dean, M.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1996) Human Genetics Section, National Cancer
Institute, NCI-FCRDC, Frederick, MD 21702, USA
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RESULT 6

CD250953

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD250953 850 bp mRNA linear EST 22-MAY-2003
AGENCOURT 14214041 NIH_MGC_179 Homo sapiens cDNA clone
IMAGE30385589 5', mRNA sequence.

CD250953

CD250953.1 GI:31011419

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM452 row: o column: 06

High quality sequence stop: 719.

FEATURES

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ORIGIN

Query Match 12.8%; Score 837; DB 6; Length 850;
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 Db 481 GAGGACAGGCTGTCTGTGATCGAGTACGTATCATGTTGCTGGGAGTTAAGATGATC 540
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 Db 841 GAACAGAGG 850
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 LOCUS CD629433 838 bp mRNA linear EST 12-JAN-2004
 DEFINITION S6046165U1 FLP Homo sapiens cDNA, mRNA sequence.
 CD629433
 ACCESSION
 VERSION CD629433.1 GI:40277699
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 838)
 AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
 TITLE Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes
 JOURNAL Genomics 84 (1), 205-210 (2004)
 COMMENT Contact: Fu GK
 Incyte Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com.
 FEATURES
 Location/Qualifiers
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 /clone_lib="FLP"
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 Db 598 GTTCAGATTTTATGTTTTGTTTGTTCATCACTCTTTTAAAGATGCTGTGTTCCCATCAA 539
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 QY 3813 CAGAACATAATGGTGCAGATGATTAAATGACAGTGAATGTATCCGTGGCTCCCATAGT 3872

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 Db 238 TTAATGTGACTGAACCAATCAGATCTGGAGTACCCCAATCTTTTCAAGAAATTAATGAT 179
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 Db 178 ATAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCAATGTTACTGCA 119
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 QY 4173 CTAAACTTTGAGTCTTTTGGCATCTGCATATGGATTGCAAGCTGTTGTTGATA 4230
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RESULT 8

B0722933 872 bp mRNA linear EST 16-JUL-2002
 LOCUS AGENCOURT_8100461 Lupski_sympathetic_trunk Homo sapiens cDNA clone
 DEFINITION IMAGE:6190464 5', mRNA sequence.

ACCESSION B0722933

VERSION B0722933.1 GI:21861819

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing Arrayed By: The I.M.A.G.E. Consortium (LLNL)

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLM13589 row: f column: 01

High quality sequence stop: 717.

Location/Qualifiers

FEATURES

source

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 5'-GACTAGTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.9 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

College of Medicine); available through Life
 Technologies."

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Gaps	7;					
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QY 5090	AGATTAATTTCTCAGAGACAGTGAAGATGATGATCTCACTGAAAGTGTATGGGTACTGTCTC	5149				
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QY 5747	TTCAATATCTTTTAA--GCTGGAGAGAGCTTAAACAT-GCTTTTGCCATTGAAGAT	5802				
Db 781	TTCAATATCTTTTAAAGCCTGGAAGAGCTTAAACATGCTTTTGCCATTGAAGAA	840				
QY 5803	ATA 5805					
Db 841	ATA 843					

RESULT 9

BC029426

LOCUS

DEFINITION Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 5,
 809 bp mrna linear HTC 19-NOV-2003
 BC029426

mRNA (cDNA clone IMAGE:4723522), containing frame-shift errors.
 BC029426
 VERSION BC029426.1 GI:20809520
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 809)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S.S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smalish, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 22388257
 12477932
 2 (bases 1 to 809)
 Strausberg, R.
 Direct Submission
 Submitted (01-MAY-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdpaxil@stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 41 Row: 1 Column: 5
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 27262625
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FEATURES

source

ORIGIN

Query Match 11.7%; Score 760.6; DB 3; Length 809;
 Best Local Similarity 99.5%; Pred. No. 1.9e-148;
 Matches 763; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 10

AY414282

LOCUS

DEFINITION

Homo sapiens ABCA9 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION

AY414282.1 GI:39770244

VERSION

Homo sapiens (human)

KEYWORDS

Homo sapiens

SOURCE

Homo sapiens

REFERENCE

1 (bases 1 to 4620)

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, F.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE

Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 4620)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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 Matches 2433; Conservative 0; Mismatches 2071; Indels 346; Gaps 19;
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 QY 1686 GTTATAGCAATTTTACCTTTTGGATACCTTTTGGCAATTCATATCGTAGCAGAAAAAGAA 1745
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 QY 1926 TATGATTAATCATCTGATTTTCTTAAATGCTGACACCTCTTTTAAATAAATCAAAA 1985
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 DB 1165 CACTTGGATCTTCAAAAATCCATACCTCATATAGTACTCTTTTCTGTTGGTTTTT 1224
 QY 2226 AATAGTATTTCTATGCTCTGCTGCTGCTATCTTCTGATCAAGTCATTTCCAGGGGATTT 2285
 DB 1225 GACACCTTCTGTATTTGGTATTTGACATATATTTGACAAATTTTGGCCGCTGAATAT 1284
 QY 2286 GCTTACCGAGATCATCTTTATTTTCTGAAGCTTCTATTTGGTCAAGAGATAAAGA 2345
 DB 1285 GGACATCATGTTCTCTGTTTCTGAAATCTGTTTGGTTTCAACGGAAGG 1344
 QY 2346 AATTATGAGGATTTACAGAGGCAATGTTAATGGAATATTAGTTTGTAGTGAATATT 2405
 DB 1345 GCTAATCATGTTGGTCTTGTAGAAATGAACAGATTTCTGATCTCTACACTAATGACTGTTT 1404
 QY 2406 GAGCAGTCTTCTTCTGAGAAATTTGTAGGAAAAAGAACCAATAAGAAATTTAGTGTATTCAAG 2465
 DB 1405 GAACAGTGTCTCCAGAAATTTCTGTGGAAAGAACCAATCAGGCCAGGTG----- 1453
 QY 2466 ACATACAGAAAGAGGTGAAATGTGGAGCTTTGAGAAATTTGTCATTTGACATATAT 2525
 DB 1454 -----TGGTGTGTGACATATAT 1470
 QY 2526 GAGGTCAGATTACTGCTTTACTTTGGCCACAGTGGAAACAGGAAAGAGTACATTGATGAAT 2585
 DB 1471 GAAGCCAGATCACTGCCCTCTTGGTCAAGTGGAGCTGGAATAACTACCTGTTAAAC 1530
 QY 2586 ATCTTTGTGACTCTGCCACCTTCTGTATGGGTTTGCATCTATATATGACACAGATC 2645
 DB 1531 ATACTTAGTGGTTGTGAGTCCAACTCAGGTTCAAGTCTGCTGTATATATCAACACT 1590
 QY 2646 TCAGAAATAGATGAATGTTTGAAGCAAGAAATGATTTGGCATTTTGTCCACAGTTAGAT 2705
 DB 1591 TCAAGATGGCTGATATAGAAATATCAGCAAGTTCATGATTTTGTCCACATCCAAT 1650
 QY 2706 ATACACTTTGATTTTGGACAGTAGAAGAAATTTATCAATTTTGGCTTCAATCAAGGG 2765
 DB 1651 GTGCAATTTGGATTTCTCACTGTGAAAGAAACCTCAGGCTGTTTGTCTAAATATAAAGGG 1710
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 DB 1711 AT-----TTTGCCACATGATGAGAA----- 1733

Qy	2826	ACTATCAAGATAACCAAGCTAAAAAAATTAAGTGGTGGTCAAAAAAGAAAGCTGTCTCAATTA	2883
Db	1734	-----	1733
Qy	2886	GGAATTGCTGTTCTTTGGGAACCCAAAGATACTGCTGCTAGATGAACCAACAGAGCTGGAATG	2945
Db	1734	-----AGAGTTTTGCTATTGGATGAACCGACTGCTGGATTG	1770
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Db	1771	GATCCTCTTTCAAGCCACCGAATATGAAATCTCTGAAAGAGGGGAATCAGACAGAGTA	1830
Qy	3006	ACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTGCAGATAGGAAGCTGTG	3065
Db	1831	ATTCTCTTCAGACCCAGTTTATAGATGAGGCTGACATTCGCGGACAGGAAGTGTTC	1890
Qy	3066	ATATCAACAAGGAATGCTGAAATGTGTGTTCTTCAATGTGTTCTCAAAAGTAAATGGGGG	3125
Db	1891	ATATCCAATGGGAAGCTGAAGTGTGAGGCTCTTCTCTGTTCTTAAAGAAGAAATGGGGC	1950
Qy	3126	ATCGGCTACCGCTGAGCATGTATACAGACAAATATTGTGCCACAGAAATCTCTTTCTTCA	3185
Db	1951	ATAGGCTACCAATTTAAGTTTTCATCTGAATCAAAAGGTGTGATCCAGAGAGTAATAACATCA	2010
Qy	3186	CTGTTTAAACAAACATATACCTGGAGCTACTTTATTACAAAGAGATGACCAACACTTGTG	3245
Db	2011	CTGGTTAAGCAGACATCTCTGATGCCAAATTGCAGCACAAGAGTGAAGAAAACCTTGTA	2070
Qy	3246	TATAGCTTGCTTTCAAGGACATGGAACAAATTTTCAGGTTTGTCTCGCCCTAGACAGT	3305
Db	2071	TATATTTTGGCTTTGGAAGACAAAACAAATTTCCAGNNNNNNNNNNNNNNNNNNNN	2130
Qy	3306	CATTCAAATTTGGGTGTCATTTCTTATGTGGTGTTCATGTACGACTTTTGGGAAGACGTATTT	3365
Db	2131	TGTTCTAACCAAGCATTGAGGATATGGTGTTCATACCAACTTTGAATGAGGTGTTT	2190
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Qy	3606	TTGCTTCTGCTTTTAATTTTTCACAGTTTCAGATTTTATGTTTTTGGTTTCATCTCT	3665
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Qy	3666	TTTAAAAATGCTGTGGTTTCCCACTAAACTTTGTTTCCAGACTTATATTTCTPAAACCTGGA	3725
Db	2488	TATCAGAAAAAGT---TACCCGTGGGAACTGTCTCCAAATACATACTCTCTCACCAGGA	2544
Qy	3726	GACAAACCAATAAATACAAACAGTCTGCTTCTTCAAATTTCTGCTGACTCAGATATC	3785
Db	2545	CAACAACCAAGGATCCTCTGACCCATTACTGGTCAATCAATGAAGACAGGTCACACATT	2604
Qy	3786	AGTGATCTTATTAGCTTTTTCACAAGCCAGAACATAATGGTGAATGATGATTAATGACAGT	3845
Db	2605	GATAAATCTTTTACATTCACCTGAGCGACAGAACATAGCTATAGAAGTGGATGCTTTGGA	2664
Qy	3846	GACTATGTATCCGTGGCTCCCATGTATGCGGCTTTAAATGTGATGCAATTCAGAAAAAGGAC	3905
Db	2665	ACTAGAAAATGGCACAGATGACCCCATCTTCAATGGTGGCTATCATTTGTGCAGGTGATGAA	2724
Qy	3906	TATGTTTTTGGCACTGTTTTCAACAGTACTATGGTTTTATTTCTTTTACCTATATTAGTGAAT	3965

[illegible]

Db 3703 -----GAAGTTATAGGACTGTGTAGGACACAATGGAGCTGGTAAAGTACACTATTA 3754
 Qy 5041 ATATCTGTTGGTGTATATGAACCACTTCAGGCCAGGTATTTTAGGAGATTATCTT 5100
 Db 3755 AGATGATACTGGAGACACAAAACCACTTCAGGACAGGTGATTTTGAAGGG----- 3807
 Qy 5101 CAGAGACAAGTGAAGATGATATTCAGTGAAGTGTATGGTACTGCTCCTCAGATAACC 5160
 Db 3808 -----AGCGTGGAGGGGAACCCCTGGGCTTCTGGGTACTGCCCTCAGGAGATG 3859
 Qy 5161 CTTTGTGGCAGATACTACATTGCAGGACATATTTTGAATTTATGGAGCTGTCAAGGAA 5220
 Db 3860 CGCTGTGGCCCAACCTGACAGTGAGGACACCTGGAGGTGTACGCTCCGCTGAAAGTC 3919
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 Qy 5521 CTATCATGTGTCTGGCGAGTTAAGATGTATCGGAACAGTACAAATCTAAAGAGTAAAT 5580
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 Qy 5581 TTGGAAAGGCTACTTTTGGAAATTAATTAAGAGCTGATGAGAAACCTTAGAAGTAG 5640
 Db 4280 TTGGCAAGACACTCTGCTGGAGATGAAGCTGAAGAACTGGGCACAA-----TGG 4330
 Qy 5641 ACCGCTTCAAGAGAAATTCAGTATATTTTCCCAATGCAAGCGCTCAGGAAAGTTT 5700
 Db 4331 AGCCCTCCATGCAGAGATCCTGAGGCTTTTCCCGCCAGCTGCTCAGCAGGAAGTTCT 4390
 Qy 5701 CTCTATTTTGGTTATAAAATTCCTAAGGAAGATGTTCACTCCCTTTCACAACTTTT 5760
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 Qy 5761 TTAAGCTGAAGAAGCTAAACATGCTTTTGCATTGAAGAATAAGCTTTTCTCAAGCAA 5820
 Db 4451 TCAAATTAGATAGTTAAACAGAGTTTCGACCTGGAGGATCAGCTCTCAGAGTCTA 4510
 Qy 5821 CATTGGAACAGGTTTTTGTAGAACTCCTAAAGAAACAGAGAGAGAT 5870
 Db 4511 CCTGGAGCAGGTTTTTCTGGAGCTCTCCAAGGAGCAGGAGCTGGTGAT 4560

RESULT 11

BQ441353

LOCUS

BQ441353 738430 NIH_MGC_82 Homo sapiens linear EST 24-MAY-2002

DEFINITION

5', mRNA sequence.

ACCESSION

BQ441353

VERSION

BQ441353.1

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 773)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.TITLE
JOURNAL
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: CLONTECH
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2334 row: c column: 01
 High quality sequence stop: 537.
 Location/Qualifiers

FEATURES
source

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 sequence: 5'-CACGCCATTATGCCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."

ORIGIN

Query Match 11.4%; Score 741.4; DB 5; Length 773;
 Best Local Similarity 98.4%; Pred. No. 2e-144;
 Matches 759; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy 5323 AACGAAAGTTGTTTCTCTTAAGTATGCTAGGAAATCCTCAGATTACTTTGCTAGATG 5382
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 Qy 5383 AACCATCTACAGTATGGATCCAAAGCCAAACAGCACATGTGGCGAGCAATTCGAAGCTG 5442
 Db 63 AACCATCTACAGTATGGATCCAAAGCCAAACAGCACATGTGGCGAGCAATTCGAAGCTG 122
 Qy 5443 CATTTAAACACAGAAAGCGGCTGTTATCTGACCACTCACTATATCGAGAGGACAGG 5502
 Db 123 CATTTAAACACAGAAAGCGGCTGTTATCTGACCACTCACTATATCGAGAGGACAGG 182
 Qy 5503 CTGCTGTGATCGAGTAGCTATCATGTGCTGGCGAGTTAAGATGTATCGGAACAGTAC 5562
 Db 183 CTGCTGTGATCGAGTAGCTATCATGTGCTGGCGAGTTAAGATGTATCGGAACAGTAC 242
 Qy 5563 AACATCTAAGAGTAAATTTGGAAAGGCTACTTTTGGAAATTAATTTGAAGACTGGA 5622
 Db 243 AACATCTAAGAGTAAATTTGGAAAGGCTACTTTTGGAAATTAATTTGAAGACTGGA 302
 Qy 5623 TAGAAAACTAGAGTAGACCGCCTTCAAGAGAAATTCAGTATATTTTCCCAAATGCAA 5682
 Db 303 TAGAAAACTAGAGTAGACCGCCTTCAAGAGAAATTCAGTATATTTTCCCAAATGCAA 362
 Qy 5683 GCGGTCAAGAAAGTTTCTTCTATTTTGGCTTATAAAATTCCTAAGAGATGTTTCAGT 5742
 Db 363 GCGGTCAAGAAAGTTTCTTCTATTTTGGCTTATAAAATTCCTAAGAGATGTTTCAGT 422
 Qy 5743 CCCTTTTCAATCTTTTTTAAAGCTGAAGAAAGCTAAACATGCTTTTGCATTGAAGAT 5802
 Db 423 CCCTTTTCAATCTTTTTTAAAGCTGAAGAAAGCTAAACATGCTTTTGCATTGAAGAT 482
 Qy 5803 ATAGCTTTTCTCAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTATAAGACAGAGG 5862
 Db 483 ATAGCTTTTCTCAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTATAAGACAGAGG 542

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QY 5863 AGGAAGATATAGTGTGGAACTTTAAACAGACACACTTTGGTGGGAAAGCAACACAAAG 5922
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QY 5923 ATAGAGTAGTATTTTCAAAATTTGATTTGTTTGGTCTGCTTACTGGGACTTCTTTCTTTTC 5982
Db 603 ATAGAGTAGTATTTTCAAAATTTGATTTGTTTGGTCTGCTTACTGGGACTTCTTTCTTTTC 662
QY 5983 ACTTAATTTTAACTTTGGTTTAAAAAGTTTTTTTATTGGAATGGTAACCTGGAGAACAAAGA 6042
Db 663 ACTTAATTTT-AACTTTGGTTTAAAAAGTTTTTTTATTGGAATGGTAACCTGGAGAACCCAGA 721
QY 6043 ACCCACTTCGAATTTTCTAAGCTCTCTAATTAATGAATGCTGTTGGTGTG 6093
Db 722 ACCCACTTCGAATTTTCTAAGCTCTCTAATTAATGAATGCTGTTGGGTTGGG 772

RESULT 12
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LOCUS 874 bp mRNA linear EST 12-JAN-2004
DEFINITION S6046273J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629439
VERSION CD629439.1 GI:40277705
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
JOURNAL Circular rapid amplification of cDNA ends for high-throughput
COMMENT extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
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1. .874
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Best Local Similarity 95.8%; Pred. No. 3.6e-144; Indels 9; Gaps 8;
Matches 846; Conservative 0; Mismatches 28;

QY 3348 ACTTTGGAAGAGCTATTTTAAAGCTAGAGTTGAAGCAGAAATTTGACCAAGCAGATTAT 3407
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QY 3408 AGTGATTTTACTCAGGAGCCACTGGAGGAGAAATTTGATTTCAAAATCTTTTGATGAATG 3467
Db 816 AGTGATTTTACTCAGCACCCTGGAGGAGAAATTTGATTTCAAAATCTTTTGATGAATG 757
QY 3468 GAACAGAGCTTACTTATTTCTTCTGAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTT 3527
Db 756 GAACAGACTTTACTTATTTCTTCTGAACCAA-GCTGCTCTAGTA-CACCATGAACTT 699
QY 3528 TGAACAACACAGATGATACATAGCAAGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3587
Db 698 TGAACAACACAGATGATACATACACAGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 639
QY 3588 AAATCAGTCAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATG 3647
Db 638 AAATCAGTCAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATG 579
QY 3648 TTTTGGTTTCATCCTCTTTTAAATGCTGGTTCCTCAATCAAACTTTGTTCCAGACTTA 3707

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Db 578 TTTTGGTTTCATCCTCTTTTAAATGCTGTGGTTCCTCCATCAAACTGTTTCAGACTTA 519
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Db 518 TATTTTCTAAAACTGGAGAC-AAACCAATAAATAAATAAATAAATAAATAAATAAATAAATAA 461
QY 3768 TCTGCTGACTCAGATCAGTGTGCTTATTTAGCTTTTTCACAGCCAGACATAAATGGTG 3827
Db 460 TCTGCTGACTCAGATCAGTGTGCTTATTTAGCTTTTTCACAGCCAGACATAAATGGTG 401
QY 3828 ACGATGATTAATGACAGTGTGCTATGATCGTGGCTCCCATAGTGGCTTTAAATGTG 3987
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QY 3888 ATGCATTCAGAAAAGGACTATGTTTTCAGCTGTTTTCACAGTACTGTTTATTTCT 3947
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QY 3948 TTACCTATATTAGTGAATATCATTTAGTAATCTATCTTTTATCATTTAAATGTGACTGAA 4007
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QY 4008 ACCATCCAGATCTGGAGTACCCCATCTTTTCAAGAAATTTACTGATATAGTTTAAAAAT 4067
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QY 4068 GAGCTGTATTTTCAAGCAGCTTTTGGAAATCATTTGTTTACTGCAATGCACTTACTTTT 4127
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QY 4128 GCCATGAAAATCCAGAGAAATCATAAGATCAAGCTTTTACTCAACTTAACTTTTCAAGT 4187
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QY 4188 CTTTGGCCATCTGCATATTGGATTGGACAGAGCTGTTGTTGATA 4230
Db 42 CTTTGGCCATCTGCATATTGGATTGGAC-AGCTGTTGTTGATA 1

RESULT 13
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LOCUS 912 bp mRNA linear EST 12-JAN-2004
DEFINITION S604640J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629443
VERSION CD629443.1 GI:40277709
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
JOURNAL Circular rapid amplification of cDNA ends for high-throughput
COMMENT extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
source
1. .912
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/note="Vector: pDrive Cloning Vector"

ORIGIN
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Best Local Similarity 96.8%; Pred. No. 1.9e-143;
Matches 869; Conservative 0; Mismatches 17; Indels 12; Gaps 11;

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D5 447 TATTTTGGCTTATAAAATTCCTAAGAGATGTTAGTCCCTTTTCCATCTTTTAA 388
QY 5765 GCTGGAAGAGCTAAACATGCTTTTGGCCATTCAAGATATAGCTTTTCTCAAGCAACAT 5824
D5 387 GCTGGAAGAGCTAAACATGCTTTTGGCCATTCAAGATATAGCTTTTCTCAAGCAACAT 328
QY 5825 GGAACAGGTTTGTAGAACTCACTAAAGAACAGAGAGGAGATATAGTGTGGAAC 5884
D5 327 GGAACAGGTTTGTAGAACTCACTAAAGAACAGAGAGGAGATATAGTGTGGAAC 268
QY 5885 TTTAAACACACACTTTTGTGGGAGAGAACACACAGAGATAGTAGTATTTTGAATTTG 5944
D5 267 TTTAAACACACACTTTTGTGGGAGAGAACACACAGAGATAGTAGTATTTTGAATTTG 208
QY 5945 TATTTGTCGCTGCTTACTGGACCTTTCTTTTCACTTTAACTTTTGGTTTA 6004
D5 207 TATTTGTCGCTGCTTACTGGACCTTTCTTTTCACTTTAACTTTTGGTTTA 148
QY 6005 AAAAGTTTTTATGGAATGTTAACTGGAGAACCAAGACGACTGAAATTTTCTTAAG 6064
D5 147 AAAAGTTTTTATGGAATGTTAACTGGAGAACCAAGACGACTGAAATTTTCTTAAG 88
QY 6065 CTCCTTAAATGAAATGCTGTGCTGTGCTTTTGTGCTTTTCTTTAAATAAAGATGAT 6124
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D5 27 AATTAAGTAA 17
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RESULT 15

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VERSION CF272622.1 GI:50872859
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 730)
AUTHORS The Transcription Finishing Consortium
http://200.18.51.201/transcript/
TITLE A transcript finishing initiative for closing gaps in the human
transcriptome
JOURNAL Genome Res. 14 (7), 1413-1423 (2004)
COMMENT Contact: Anamaria Aranha Camargo
Laboratory of Molecular Biology and Genomics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente, 109, 4th floor-01509-010 SP Brazil
Tel: (55) 011 33883248
Fax: (55) 011 32077001
Email: anamaria@compbio.ludwig.org.br
RT-PCR fragment amplified from a pool of cDNAs prepared from tumor
cell lines.
PCR Primers
FORWARD: gccacaaagggtttatctatgc
BACKWARD: gcagcgtggcttgcattgc
POLYA=No.
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FEATURES

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human transcripts. Using the genomic sequence as a
scaffold for EST mapping and clustering we have performed
RT-PCR to bridge gaps between EST clusters that are likely
to be derived from the same genes. Each pair of EST
clusters selected for experimental validation was
designated a single Transcript Finishing Unit (TFU). In
this way we are able to confirm the membership of ESTs
from different clusters to a common transcript and to
provide intervening sequence information."
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ORIGIN

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Query Match 11.2%; Score 729; DB 6; Length 730;
Best Local Similarity 99.9%; Pred. No. 7.9e-142;
Matches 729; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4440 GCAGCGTTCGCTTGTATTCGCAATCAGTGAATAAATCTTTTATGGGATACAAATGCA 4499
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QY 4500 ACTATTCTTCATTCAGCTTTCGCTTGTATTCATCATTCCCAATCTATCCACTTCTAGTTCCTG 4559
D5 61 ACTATTCTTCATTCAGCTTTCGCTTGTATTCATCATTCCCAATCTATCCACTTCTAGTTCCTG 120
QY 4560 ATTTCTTTTCATAAGAGATTTCTTGGAAAGATGTACGAAAAAATGTGGACACCTATATCA 4619
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QY 4620 TGGGATAGGCTTTCAGTAGCTGTATATCGCCTTACCTGAGTGTCTACTGTGGATTTTC 4679
D5 181 TGGGATAGGCTTTCAGTAGCTGTATATCGCCTTACCTGAGTGTCTACTGTGGATTTTC 240
QY 4680 CTCTTCAATATCTATGAGAAAAAATATGGAGGACAGATCAATAAGAAAAAGATCCCTTTTTC 4739
D5 241 CTCTTCAATATCTATGAGAAAAAATATGGAGGACAGATCAATAAGAAAAAGATCCCTTTTTC 300
QY 4740 AGAAACCTTTTCAACGAGTCTTAAATATAGAGAGTCTCCAGAACCCAGACCAATGAGAT 4799
D5 301 AGAAACCTTTTCAACGAGTCTTAAATATAGAGAGTCTCCAGAACCCAGACCAATGAGAT 360
QY 4800 GAAGATGAAGATGCTCAAGCTGAAGACTAAAGTCAAGAGCTGATGGTTGCCAGTCT 4859
D5 361 GAAGATGAAGATGCTCAAGCTGAAGACTAAAGTCAAGAGCTGATGGTTGCCAGTCT 420
QY 4860 TGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGTCATAAAGAAATATGATGACAAGAAA 4919
D5 421 TGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGTCATAAAGAAATATGATGACAAGAAA 480
QY 4920 GATTTCTCTTTTCAAGAAAAAGTAAAGAGTGGCAACTTAAATACATCTCTTCTGTGG 4979
D5 481 GATTTCTCTTTTCAAGAAAAAGTAAAGAGTGGCAACTTAAATACATCTCTTCTGTGG 540
QY 4980 AAAAAAGGAGAGATCTTAGGACTTATGGTCCAAATGGTGGCAAAAAGCAATTAAT 5039
D5 541 AAAAAAGGAGAGATCTTAGGACTTATGGTCCAAATGGTGGCAAAAAGCAATTAAT 600
QY 5040 AATATTCTGGTGGTGAATATTAACCACTTACGCCAGGTATTTTAGAGATATTCT 5099
D5 601 AATATTCTGGTGGTGAATATTAACCACTTACGCCAGGTATTTTAGAGATATTCT 660
QY 5100 TCAGAGACCAAGTGAAGATGATGATTCACCTGAAGTGTATGGGTACTGTCTCAGATAAAC 5159
D5 661 TCAGAGACCAAGTGAAGATGATGATTCACCTGAAGTGTATGGGTACTGTCTCAGATAAAC 720
QY 5160 CCTTTGTGGC 5169
D5 721 CCTTTGTGGC 730
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Search completed: December 4, 2004, 19:35:19

Mon Dec 6 10:08:10 2004

Job time : 18062 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2004, 06:19:06 ; Search time 459 Seconds
(without alignments)
9888.907 Million cell updates/sec

Title: US-10-005-338B-1
Perfect score: 6525
Sequence: 1 aaatgttgatattttctt.....ttgatcataataagtgaat 6525

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	4.9	485	US-09-621-976-409	Sequence 409, App
2	159.2	2.4	5894	US-08-685-259-24	Sequence 24, Appl
3	159.2	2.4	5894	US-08-762-500-24	Sequence 24, Appl
4	159.2	2.4	6525	US-08-762-500-74	Sequence 74, Appl
5	137.6	2.1	7860	US-09-526-193A-2	Sequence 2, Appl
6	121.8	1.9	8037	US-09-774-528-209	Sequence 209, App
7	108.6	1.7	6705	US-09-032-438C-5	Sequence 5, Appl
8	108.6	1.7	6819	US-09-032-438C-2	Sequence 2, Appl
9	108.6	1.7	7488	US-09-032-438C-1	Sequence 1, Appl
10	105.6	1.6	786431	US-09-751-389-3	Sequence 3, Appl
11	103.4	1.6	1064	US-08-858-207A-88	Sequence 88, Appl
12	92.2	1.4	954	US-08-858-110-2618	Sequence 2618, Ap
13	92.2	1.4	5625	US-08-961-537-1	Sequence 1, Appl
14	83.8	1.3	450	US-09-621-976-2582	Sequence 2582, Ap
15	83.8	1.3	463	US-09-621-976-2581	Sequence 2581, Ap
16	83.4	1.3	478	US-09-621-976-2583	Sequence 2583, Ap
17	80.6	1.2	795	US-08-961-527-264	Sequence 264, App
18	79.6	1.2	750	US-09-583-110-876	Sequence 876, App
19	77.8	1.2	8536	US-08-956-171E-278	Sequence 278, App
20	77.8	1.2	8536	US-08-781-986A-278	Sequence 278, App
21	77.2	1.2	696	US-09-134-001C-987	Sequence 987, App
22	76.8	1.2	3044	US-09-710-279-4290	Sequence 4290, Ap
23	75.8	1.2	1026	US-09-134-001C-1205	Sequence 1205, Ap
24	75.8	1.2	1026	US-09-710-279-3201	Sequence 3201, Ap
25	75	1.1	774	US-09-107-532A-412	Sequence 412, App
26	74.6	1.1	1664976	US-08-916-421B-1	Sequence 1, Appli
27	74.6	1.1	1664976	US-09-692-570-1	Sequence 1, Appli

28	72.2	1.1	768	4	US-09-107-532A-1681	Sequence 1681, Ap
29	71.6	1.1	819	4	US-09-861-451A-3	Sequence 3, Appli
30	71	1.1	729	4	US-09-583-110-324	Sequence 324, App
c 31	71	1.1	1664976	4	US-08-516-421B-1	Sequence 1, Appli
c 32	71	1.1	1664976	4	US-09-692-570-1	Sequence 1, Appli
33	70.4	1.1	747	4	US-09-710-279-3217	Sequence 3217, Ap
34	70.4	1.1	4089	4	US-09-710-279-4203	Sequence 4203, Ap
35	69.8	1.1	990	4	US-09-107-532A-1190	Sequence 1190, Ap
36	69.8	1.1	28626	4	US-09-596-002-15	Sequence 15, Appl
37	69.2	1.1	969	4	US-09-107-532A-1008	Sequence 1008, Ap
c 38	68.4	1.0	19124	2	US-08-487-826B-13	Sequence 13, Appl
c 39	68	1.0	7963	4	US-08-956-171E-168	Sequence 168, App
c 40	68	1.0	7963	4	US-08-781-986A-168	Sequence 168, App
41	67.4	1.0	1011	4	US-09-583-110-366	Sequence 366, App
42	67.4	1.0	1599	4	US-09-543-681A-474	Sequence 474, App
43	66.2	1.0	714	4	US-09-134-000C-1821	Sequence 1821, Ap
44	66.2	1.0	723	4	US-09-583-110-818	Sequence 818, App
c 45	65.8	1.0	4848	4	US-08-961-527-185	Sequence 185, App

ALIGNMENTS

RESULT 1

US-09-621-976-409
; Sequence 409, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 409
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 185..484
US-09-621-976-409

Query Match	4.9%;	Score 318;	DB 4;	Length 485;
Best Local Similarity	100.0%;	Pred. No. 8.9e-66;		
Matches	318;	Conservative	0;	Mismatches
			0;	Gaps
QY	994	AGGTTTATTCAGAAAACATGTCCTCACTGCAATTAGGAGGTAGGAGTTGGACACAGACCA	1053	
Db	168	AGGTTTATTCAGAAAACATGTCCTCACTGCAATTAGGAGGTAGGAGTTGGACACAGACCA	227	
QY	1054	GAACACTTCTACTGAAGAATTTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGG	1113	
Db	226	GAACACTTCTACTGAAGAATTTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGG	287	
QY	1114	AAATCTTTTTCACATTTTTTTTTTTTATTTGGTTTAATTAATTAGCATGATGCATCCAA	1173	
Db	288	AAATCTTTTTCACATTTTTTTTTTTTATTTGGTTTAATTAATTAGCATGATGCATCCAA	347	
QY	1174	ATAAGAAATATGAGAGTGCCCTAATATAGAACTCAATCCTATGGCAAGTTTACTCTTTT	1233	
Db	348	ATAAGAAATATGAGAGTGCCCTAATATAGAACTCAATCCTATGGCAAGTTTACTCTTT	407	
QY	1234	CTAATCTAATTTCTGGATATCTCCAGTCAGTCACTAATTAATTAACAGCAGCATCATGCGAAAG	1293	
Db	408	CTAATCTAATTTCTGGATATCTCCAGTCAGTCACTAATTAATTAACAGCAGCATCATGCGAAAG	467	
QY	1294	TGCTTACTGATCATCTAC	1311	
Db	468	TGCTTACTGATCATCTAC	485	

RESULT 2

US-08-665-259-24
; Sequence 24, Application US/08665259
; Patent No. 6028173
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,259
; FILING DATE: 17-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IGS-9.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..5053
; US-08-665-259-24

Query Match 2.4%; Score 159.2; DB 3; Length 5894;
Best Local Similarity 48.0%; Pred. No. 1.2e-27;
Matches 554; Conservative 0; Mismatches 588; Indels 12; Gaps 3;
QY 2214 ATGCTCACACTTAATAGTATATTCATGTCCTCTGGCTGTCTATCTTGTATCAAGTCAAT 2273
DB 1304 ATGCTGCTGGATCTGTGCTCTATGGCTGTGTGACTGGTACATGAGCGGCTTTC 1363
QY 2274 CCAGGGAAATTTGGTTACGGAGATCATCTTTATATTTTCTGAAGCCTTTCATATGTGCA 2333
DB 1364 CCAGGGCAATTCGGCGTGCCTCAGCCCTGGTACTTCTTCATCATGCTCCCTCTATTGGTGT 1423
QY 2334 AAGAGTAAAGAAATATGAGGAGTTATCAGAGGCAATGTTAATGGAATATTAGTTT 2393
DB 1424 GGAAGCCAGGGCGGTGACGGAGGAGGAGAGACAGTACCGCCGAGAAAGCACTC 1483
QY 2394 AGTGAATATTATGAGCCAGTTTCTTCAGAAATTTGTAGAAAGAGCCATGAAGATTAGT 2453
DB 1484 AGAAACGAGTACTTTGAAGCCGAGCCAGAGGACCTGG--TGGCGGGATCAAGATCAAG 1540
QY 2454 GGTATTCAGACATACAGAAAGAGGTTGAATGTGGAGGCTTTGAGAAATTTGCA 2513

DB 1541 CACCTGTCCAAGGTGTTACGGGTGGAAATAAGGACAGGGCGCGCTCAGAGACCTGAAC 1600
QY 2514 TTTGACATATATGAGGTCAGATTACTGCTTACTTGGCCACAGTGGACACAGAAAGAGT 2573
DB 1601 CTCACCTGTACAGGAGCAGATACCGTCTCTGCTGGGCCAACAGTCCCGGAGAGACC 1660
QY 2574 ACATTGATGAATATCTTTTGTGACTCTGCCACCTTCTGTATGGTTCATCTATATAT 2633
DB 1661 ACCACCTCTCCATGCTCACAGTCTCTTTCCCCACAGTGGAGCGGCATACATCAGC 1720
QY 2634 GGACACAGAGTCTCAGAAATAGATGAATTTTGAAGCAAGAAATGATGGCATTTGT 2693
DB 1721 GGGTATGAATTTCCAG-----GACATGGTTCAGATCCGGAAGAGCCTGGGCGCTGTC 1774
QY 2694 CCACAGTTAGATATACACTTTTGTATGTTTTCAGAGTGAAGAAATTTATCAATTTTGGCT 2753
DB 1775 CCGCAGCAGCATCTCTGTTTGAACATTTGACAGTCCGAGAGCACCTTTATTTCTACGCC 1834
QY 2754 TCAATCAAGGGATACCGCCAAATATATAATACAGAAAGTCAAGAGTTTACTAGAT 2813
DB 1835 CAGCTGAAGGGCCTGTACGTCAGAGTGCCTCGAAGAGTCAAGCAGATGCTGCACATC 1894
QY 2814 TTAGACATGCAGACTATCAAGATTAACCAAGCTAAAAAATTAAGTGTGCTCAAAAAGA 2873
DB 1895 ATCGGCTGGAGCAAGTGGAACTCACGGAGCGGCTTCTGAGCGGGGCATGAGGCGC 1954
QY 2874 AAGCTGTCTATTAGGAATCTGTTCTTGGGAACCCAAAGATACTGCTGTAGATGAACCA 2933
DB 1955 AAGCTCTCCATCGGCATCGCCTCATCGCAGGCTCCAAGTCTGATCTACTGACGAGCCC 2014
QY 2934 ACAGCTGGATGGACCCCTGTTCTCGACATTTGATGAATCTTTTAAATACAGAAA 2993
DB 2015 ACCTGGGATGGACGCCATCTCCAGAGGGGCATCTGGGATCTTCTTCAGCGGAGAAA 2074
QY 2994 GCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGTGCATTTCTTCAGAT 3053
DB 2075 AGTGACCGGACCATCGTGTGCTGACCCACCTTCATGGACGAGGCTGACCTGTGGAGAC 2134
QY 3054 AGAAAGCTGTGATATCAAGAGATGCTGAATGTGTGTTCTTCAATGTTCTCTCAA 3113
DB 2135 CGCATCGCCATCATGCGCCAAAGGGGAGTGCAGTGTGCGGGTCTCGCTGTTCTCTCAAG 2194
QY 3114 AGTAAATGGGGATCGGCTACCGCTACGCTGAGCATGTACATAGACAAATATGTGCCACAGAA 3173
DB 2195 CAGAAATACGGTCCCGCTATCACATGACGCTGGTGAAGAGCCGCTGCAACCGGAA 2254
QY 3174 TCTCTTCTCTACTGTTTAAACAAATATACCTGGAGCTACTTTTATTAACAAGAAATGAC 3233
DB 2255 GACATCTCCAGCTGCTCCACCAACACCGTCCCAAGCGCCACGCTGGAGAGACGCTGGG 2314
QY 3234 CAACAACTTGTATAGTTCGCTTTCAAGGACATGGACAAATTTTTCAGTTTGTGTTTCT 3293
DB 2315 GCGAGCTGTTTCTATCTTCCAGAGAGACGACAGAGTTTGAAGTCTCTTTGCT 2374
QY 3294 GCCTAGACAGTCAATCAAAATTTGGTGTCAATTC---TTATGGTGTTCATGAGACT 3350
DB 2375 AAATCGGAGAGAGCAGAAAGAGCTGGGCAATTCGAGCTTTGGGSCATCCATCACCACC 2434
QY 3351 TTGGAAGAGTATT 3364
DB 2435 ATGGAGGAAGTCTT 2448

RESULT 3

US-08-762-500-24
; Sequence 24, Application US/08762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.

APPLICANT: Klinger, Katherine W.
 TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
 TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
 NUMBER OF SEQUENCES: 83
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENZYME CORPORATION
 STREET: One Mountain Road
 CITY: Framingham
 STATE: Massachusetts
 COUNTRY: United States of America
 ZIP: 01701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/762,500
 FILING DATE: 09-DEC-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/665,259
 FILING DATE: 17-JUN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/10469
 FILING DATE: 17-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Dugan, Deborah A.
 REGISTRATION NUMBER: 37,315
 REFERENCE/DOCKET NUMBER: IGS-9.3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (508) 872-8400
 TELEFAX: (508) 872-5415
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5894 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 2..5053
 US-08-762-500-24

	Query Match	2.4%	Score 159.2	DB 3	Length 5894
	Best Local Similarity	48.0%	Pred. No. 1.2e-27	Indels 12	Gaps 3
	Matches 554	Conservative	0	Mismatches 588	
QY	2214	ATGCTCACACTTAATAGTATATCTATGTCCTCTTGCTGTCTCTATCTTGCTGTCTCTATCTTGATCAAGTCATT	2273		
DB	1304	ATGCTGCTGCTGACTCTGTGCTCTATGGCTGTGTGACCTGTGTACATGGAGGCGGCTCTTC	1363		
QY	2274	CAAGGGGAATTTGGCTTACGGAGTCATCTTTATATTTCTGAAGCCTTCATATTCGTCA	2333		
DB	1364	CCAGGGCAGTTCCGGCGTCCCTCAGCCCTGGTACTTCTTCATCATGCTCTCTATTTGGTGT	1423		
QY	2334	AAAGAGTAAAAGAAATATATGAGGAGTTATCAGAGGGCAATGTAATGGAATATATTAGTTTT	2393		
DB	1424	GGGAGCCAGGGCGGTTGCAGGGAAGGAGGAGACAGTACCCTCCGAGAAGCACTC	1483		
QY	2394	AGTGAATATTATGAGCCAGTTTCTTCAGATTTTGTAGGAAAGNAGCCATAAGATTAGT	2453		
DB	1484	AGAAACGAGTACTTTTGAAGCCGAGCCAGAGACCTCG--TGGCGGGGATCAAGATCAAG	1540		
QY	2454	GGTATTTCAGAAAGACATACAGAAAGAGGGTGAAATGTGGAGGCTTTGAGAAATTTGTCA	2513		
DB	1541	CACCTGTCCAAAGTGTTCAGGGTGGGAAATAAGGACAGGCGGCGTCAGAGACCTGAAC	1600		
QY	2514	TTTGACATATATGAGGTCAGATTACTTGCCTTACTTGGCCACAGTGGAAAGCAAGAGT	2573		
DB	1601	CTCAACCTGTACGAGGACAGATCACCGTCTGCTGGGCCACACACGGTGGCGGAAGACC	1660		

RESIT.T 4

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US-08-762-500-74
; Sequence 74, Application US/08762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-526-193A-2

Query Match      2.1%; Score 137.6; DB 4; Length 7860;
Best Local Similarity 52.7%; Pred. No. 1.7e-22;
Matches 349; Conservative 0; Mismatches 304; Indels 9; Gaps 2;

QY 2492 GGAGGCTTTGAGAAATTTGTCATTTGACATATATGAGGTCAGATTACTGCTTACTTGG 2551
Db 2813 GGTGGCTGTCGATGGCTGGCACTGAATTTTATGAGGCCAGATCACCTCTCTCTGGG 2872
QY 2552 CCACAGTGGACAGGAAGTAGTACATGTAGATATTTTGGGACTCTGCCACCTTC 2611
Db 2873 CCACATGAGGCGGGGAGACGACCCATGTCAATCCTGACCGGGTTGTCCTCCCGAC 2932
QY 2612 TGATGGTTTGCATCTATATATGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGC 2671
Db 2933 CTCGGGCACCGCTACATCTCTGGGAAAGACATTGGCTC-----TGAGATGAGCACCAT 2986
QY 2672 AAGAAATGATTGGCATTTGTCTCAGAGTTAGATATACATTTTGATGTTTTCAGATAGA 2731
Db 2987 CCGGCAGAACCTGGGGGTCTGTCCCCAGCATACGCTGCTGTTGACATGCTGACTGTGGA 3046
QY 2732 AGAAATTTTATCAATTTTGGCTTCAATCAAGGGATACACGCAACAATATATACAAGA 2791
Db 3047 AGAACATCTGTTCTATGCCCGCTTGAAGGGCTCTCTGAGAGCACCTGAAGCGGA 3106
QY 2792 AGTCAGAGGTTTACTAGATTTAGACATGTCAGACTATCAAA---GATAAACCAAGTAA 2848
Db 3107 GATGAGCAGATGGCCCTGGATGTTGGTTTGGCCATCAAGCAAGCTGAAAGCAAAACAAG 3166
QY 2849 AAATTAAGTGGCTGCTCAAAAGAAAGCTGTCAATTAGGAATTGCTCTCTCTGGGAACCC 2908
Db 3167 CCAGCTGTGAGTGAATGACAGAAAGCTATCTGTGGCTTGGCCCTTGTCTGGGGATC 3226
QY 2909 AAAGATCTGTCTGTAGATGAACCAACAGCTGGAATGAGCCCTGTTTCTCGACATATTGT 2968
Db 3227 TAAGTTTGTCAATCTGGATGAACCCACAGCTGGTGTGGACCCCTTACTCCCGGAGGGAAT 3286
QY 2969 ATGGAATCTTTTAAATATACAGAAAGCAATCGGGTACAGTGTTCAGTACTCATTTTCAT 3028
Db 3287 ATGGAGCTGTCTGTAATACCGACAAAGCGCCGACCATATTATCTCTCTACACACACAT 3346
QY 3029 GGATGAAGCTGACATTTCTTGACAGATAGGAAGCTGTGATATCAAGGAATGCTGAAATG 3088
Db 3347 GGATGAAGCGGACGTCTCTGGGGGACAGATTGCCATCATCTCCATCGGAAGCTGTGCTG 3406
QY 3089 TGTTGGTTCTTCAATGTTCTCAAAAGTAAATGAGGGGATCGGCTACCGCTGAGCATGTA 3148
Db 3407 TGTGGCTCTTCCCTGTTTCTGAAGAACCAAGCTGGGAACAGGCTACTACCTGACCTTGGT 3466
QY 3149 CA 3150
Db 3467 CA 3468
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RESULT 6

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US-09-774-528-209
; Sequence 209, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyao
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
```

```

; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: Pt_Fl_genes Version 2.0
; SEQ ID NO 209
; LENGTH: 8037
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1654)..(7329)
US-09-774-528-209
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Query Match      1.9%; Score 121.8; DB 4; Length 8037;
Best Local Similarity 49.9%; Pred. No. 9.6e-19;
Matches 337; Conservative 0; Mismatches 332; Indels 6; Gaps 1;

QY 2476 AGAAGGTTGAAATGTTGAGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGTCAGA 2535
Db 2999 ACAGGAGCAGCAAGAAGCTGGCCCTGGAACAAGCTGAGCTGAACCTCTACGAGAACCCAGG 3058
QY 2536 TTACTGCTTACTTGGCCACAGTGGAAACAGGAAGAGTACATTTGATGAATATTTCTTGTG 2595
Db 3059 TGGTCTCTCTTGTGGCCACACAGCGGGCGGCAAGACCACCACCATGTCCTTCTGACCG 3118
QY 2596 GACTCTGCCACCTTCTGATGGTTTGCATCTATATATGACACAGAGTCTCAGAAATAG 2655
Db 3119 GCCTGTCTCCTCAACGCTGGGTTCCGGCCACCATCTACGGGACGACATCCGACG----- 3174
QY 2656 ATGMAATGTTTGAACCAAGAAATGATTGGCATTTGTCAGTTAGATATATACATTTG 2715
Db 3175 --GAGATGATGAGATCCGCAAGAACCTGGGCAATGTGCCGAGACACATGTGCTCTTTG 3232
QY 2716 ATGTTTTCAGTAGAAGAAATTTTCAATTTTGGCTTCAATTTAAAGGGATACAGCCA 2775
Db 3233 ACCGCTCAGCTGGGAGGAACACCTCTGTTTCTACTCAGGCTCAAGAGCATGGCTCAGG 3292
QY 2776 ACAATATATACAGAAAGTGCAGAGGTTTACTAGATTAGACATGACACTATCAAG 2835
Db 3293 AGGAGATCCGACAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAAACAAACGC 3352
QY 2836 ATAAACCAAGCTAAAAATTAAGTGGTGTCAAAAAAGAAAGCTGTCTATTAGGAATTGCTG 2895
Db 3353 ACTACTGTGACAGACATTTGTCGGGTGGCATGAGCGCAAGCTGTCCGTGGCCATCGCT 3412
QY 2896 TTCTTGGGAACCCAAAGATACCTGCTGTAGATGAACCAACAGCTGGAATGGACCCCTGTT 2955
Db 3413 TCGTGGCGGCTCTCGCGCCATCATCTCTGAGAGCCCAACGCGCGGCGTGGACCCCTAGC 3472
QY 2956 CTCGACATATTGTAGGATCTTTTAAATATACAGAAAGCCCAATCGGTTGACAGTGTTC 3015
Db 3473 CGGCGCGGCGCATCTGGGACCTCATCTCTGAAGTACAGCCAGCGCCGACCATCTCTCT 3532
QY 3016 GTACTCATTTTCATGGATGAAGCTGACATTTCTTGCAGATAGGAAGCTGTGATATCAAG 3075
Db 3533 CCACCCACCATGGATGAGGCTGACCTGTTGGGACCGCATTTGCCATCATCTCCCATG 3592
QY 3076 GAATGCTGAAATGTGTGTTGTTTCTTCAATGTTCTCAAAAGTAAATGGGGGATCGGCTACC 3135
Db 3593 GGAAGCTCAAGTGTCTCGGCTCTCCCGCTCTTCTCAAGGGCACCTTATGCGGCGGTACC 3652
QY 3136 GCCTGAGCATGTACA 3150
Db 3653 GCCTCAGCTGGTCA 3667
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RESULT 7
US-09-032-438C-5
; Sequence 5, Application US/09032438C
; Patent No. 6713300
; GENERAL INFORMATION:
; APPLICANT: Rattner, Amir
; APPLICANT: Sun, Hui
; APPLICANT: Lupski, James R.
; APPLICANT: Nathans, Jeremy
; APPLICANT: Anderson, Kent L.
; APPLICANT: Leppert, Mark
; APPLICANT: Dean, Michael
; APPLICANT: Singh, Nanda
; APPLICANT: Shroyer, No. 6713300h F.
; APPLICANT: Smallwood, Philip M.
; APPLICANT: Allikmets, Rando
; APPLICANT: Lewis, Richard A.
; APPLICANT: Li, Yixin
; TITLE OF INVENTION: Nucleic Acid And Amino Acid Sequences For ATP-Binding Cassette
; TITLE OF INVENTION: Transporter And Methods Of Screening For Agents That Modify
; FILE REFERENCE: BYLR-0065
; CURRENT FILING DATE: 1998-02-27
; PRIOR FILING DATE: 1997-02-27
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-032-438C-5

Query Match 1.7%; Score 108.6; DB 4; Length 6705;
Best Local Similarity 49.8%; Pred. No. 1.2e-15;
Matches 332; Conservative 0; Mismatches 329; Indels 6; Gaps 2;

QY 4966 TCTCTTTCTGTGTAAGGAGAGATCTTAGGACTATTGGTCCCAATGGTCTGGCA 5025
DB 5759 TGTGTGTCGAGTTCGCCCTGAGAGTGTCTTGGCTCTCTGGAGTGAATGGTCCGGCA 5818
QY 5026 AAAGCACAAATTATTAATTTCTGGTTGGTGAATTTGAACCAACTTCAGGCCAGGTATTTT 5085
DB 5819 AAACAACACATTCAGATGCTCACTGGGGACACACAGTGACCTCAGGGATGCCACG 5878
QY 5086 TAGGAGATTATTTCTCAGACAGCAAGTGAAGATGATGATCACTGAAGTGTATGGTTACT 5145
DB 5879 TAGCAGGCAAGAGTATTTTAACCAATATTTCTGAAGTCCATCAAAA---TATGGGCTACT 5935
QY 5146 GTCCTCAGATAAACCTTTGTGGCCAGATACACTACATTCAGGAAACATTTTGAATTTATG 5205
DB 5936 GTCCTCAGTTTGTGCAATCGATGAGTCTCAGAGGACGAGACATCTTTACCTTTATG 5995
QY 5206 GAGCTGTCAAAGGAATGATGCAAGTGACATGAAGAAGTCAATAGTCCAAATACACATG 5265
DB 5996 CCGCGCTTCGAGGTGTACCAGCAGAAGAAATCGAAAAGGTTGCAAACTGGAGTATTAAGA 6055
QY 5266 CACTTGATTTAAAGAACATCTTCAGAAGACTGTAAAGAACTACCTTCAGGAATCAAAAC 5325
DB 6056 GCCTGGGCTGACTGTCTACGCCGACTGCTGGCTGGCAGCTGACAGTGGGGGCAACAGC 6115
QY 5326 GAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTTTGTAGATGAAC 5385
DB 6116 GGAAGTCTCCACAGCCATCGCACTCATTTGGTGCCACCCGCTGCTGCTGCTGATGAGC 6175
QY 5386 CATCTACAGGTATGATCCCAAGCCAAACAGCACATGCTGGGAGCAATTCGAATGCAT 5445
DB 6176 CCACCACAGGGATGACCCCGCAGCCGCGATGCTGTGGAACGTCTCATCTGTGAGATCA 6235
QY 5446 TTAAAAACAGAAAGCGGGCTGTCTATTCTTGACCACTCACTATATATGAGGAGGAGGCTG 5505

Db 6236 TCAGAGA--AGGAGGGCTGTGGTCTTCACATCCACAGCATGGGAATGTGAGGCAC 6292
QY 5506 TCTGTGATCGAGTAGCTATCATGCTGTCTGGCAGTTAAGATGTATCGGAACAGTACAC 5565
DB 6293 TGTGTACCCGGCTGGCCATCATGTTAAAGCGGCCCTTCGATGTATGGSCACCATTCAGC 6352
QY 5566 ATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTAATTAAGAGCTGGATAG 5625
DB 6353 ATCTCAAGTCCAAATTTGGAGATGGCTATATCGTCACATGAAGATCAATCCCCGAGG 6412
QY 5626 AAAACCT 5632
DB 6413 ACGACCT 6419

RESULT 8
US-09-032-438C-2
; Sequence 2, Application US/09032438C
; Patent No. 6713300
; GENERAL INFORMATION:
; APPLICANT: Rattner, Amir
; APPLICANT: Sun, Hui
; APPLICANT: Lupski, James R.
; APPLICANT: Nathans, Jeremy
; APPLICANT: Anderson, Kent L.
; APPLICANT: Leppert, Mark
; APPLICANT: Dean, Michael
; APPLICANT: Singh, Nanda
; APPLICANT: Shroyer, No. 6713300h F.
; APPLICANT: Smallwood, Philip M.
; APPLICANT: Allikmets, Rando
; APPLICANT: Lewis, Richard A.
; APPLICANT: Li, Yixin
; TITLE OF INVENTION: Nucleic Acid And Amino Acid Sequences For ATP-Binding Cassette
; TITLE OF INVENTION: Transporter And Methods Of Screening For Agents That Modify
; FILE REFERENCE: BYLR-0065
; CURRENT FILING DATE: 1998-02-27
; PRIOR FILING DATE: 1997-02-27
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 6819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-032-438C-2

Query Match 1.7%; Score 108.6; DB 4; Length 6819;
Best Local Similarity 49.8%; Pred. No. 1.2e-15;
Matches 332; Conservative 0; Mismatches 329; Indels 6; Gaps 2;

QY 4966 TCTCTTTCTGTGTAAGGAGAGATCTTAGGACTATTGGTCCCAATGGTCTGGCA 5025
DB 5873 TGTGTGTCGAGTTCGCCCTGAGAGTGTCTTGGCTCTCTGGAGTGAATGGTCCGGCA 5932
QY 5026 AAAGCACAAATTATTAATTTCTGGTTGGTGAATTTGAACCAACTTCAGGCCAGGTATTTT 5085
DB 5933 AAACAACACATTTCAAGATGCTCACTGGGGACACACAGTGACCTCAGGGATGCCACG 5992
QY 5086 TAGGAGATTATTTCTCAGACAGCAAGTGAAGATGATGATCACTGAAGTGTATGGTTACT 5145
DB 5993 TAGCAGGCAAGAGTATTTTAACCAATATTTCTGAAGTCCATCAAAA---TATGGGCTACT 6049
QY 5146 GTCCTCAGATAAACCTTTTGTGGCCAGATACACTACATTCAGGAAACATTTTGAATTTATG 5205
DB 6050 GTCCTCAGTTTGTGCAATCGATGAGTCTCAGAGGACGAGACATCTTTACCTTTATG 6109
QY 5206 GAGCTGTCAAAGGAATGAGTGAAGTGAATGAAGAAGTCAATAGTGAATTAACATG 5265
DB 6110 CCGCGCTTCGAGGTGTACCAGCAGAAGAAATCGAAAAGGTTGCAAACTGGAGTATTAAGA 6169
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;; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
;; FILE REFERENCE: P400-07A
;; CURRENT APPLICATION NUMBER: US/09/583,110
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/107,433
;; PRIOR FILING DATE: 1998-06-30
;; PRIOR APPLICATION NUMBER: US 60/085,131
;; PRIOR FILING DATE: 1998-05-12
;; PRIOR APPLICATION NUMBER: US 60/051,553
;; PRIOR FILING DATE: 1997-07-02
;; NUMBER OF SEQ ID NOS: 5322
;; SEQ ID NO 2618
;; LENGTH: 954
;; TYPE: DNA
;; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2618

Query Match 1.4%; Score 92.2; DB 4; Length 954;
Best Local Similarity 46.2%; Pred. No. 3.8e-12;
Matches 307; Conservative 0; Mismatches 358; Indels 0; Gaps 0;

QY 4923 TTTCCTCTTCAAGAAAGTAAAGAGTGGCAACTAAATACATCTCTTCTGTGTA 4982
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 105
QY 4983 AAAGGAGAGATCTTAGGACTATTGGTCCAAATGGTCTGGCAAAAGCAATTTAAT 5042
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 105
QY 4983 AAAGGAGAGATCTTAGGACTATTGGTCCAAATGGTCTGGCAAAAGCAATTTAAT 5042
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 105
QY 5043 ATTCGTGGTGTGATATGACCAACTTCAGGCCAGGTATTTTAGGAGATTTCTTCA 5102
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 105
QY 5103 GAGCAAGTGAAGATGATGATCTACTGAAGTGTATGGTCTCTCTAGATAAACCTT 5162
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 105
QY 5163 TTGTGGCCAGATCTACATTTGAGCAAGATTTTGAATTTATGAGAGTGTCAAGGATG 5222
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 105
QY 5223 AGTCAAGTGAAGATGATGATCTACTGAAGTGTATGGTCTCTCTAGATAAACCTT 5162
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 105
QY 5283 CATCTTCAGAGAGTGTAAAGAACTACTCTGAGAGATCAACCGAAAGTGTGTTTGTCT 5342
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 105
QY 5343 CTAAGTATCTAGGAACTCTCAGATTTACTTTGTAGATGAACCATCTACAGGTATGAT 5402
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 105
QY 5403 CCCAAAGCCAAACAGCATGTGGCGAGCAATTCGAATCTGAACTGAACTGAAAGCGG 5462
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 105
QY 5463 GGTGCTATCTGACCACTACTATATGAGAGGAGGAGGCTGTCTGTGATCGAGTACT 5522
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 105
QY 5523 ATCATGGTCTCGGCGAGTGAAGTGTATCGGAACAGTACCACTCTAAAGAGTAAATTT 5582
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 105
QY 5583 GGAAA 5587
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 105

RESULT 13
US-08-961-527-1

;; Sequence 1, Application US/08961527
;; Patent No. 6420135
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunsch
;; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 391
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/961,527
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brookes A. Anders
;; REGISTRATION NUMBER: 36,373
;; REFERENCE/DOCKET NUMBER: PB340P1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5625 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
US-08-961-527-1

Query Match 1.4%; Score 92.2; DB 4; Length 5625;
Best Local Similarity 46.2%; Pred. No. 8.4e-12;
Matches 307; Conservative 0; Mismatches 358; Indels 0; Gaps 0;

QY 4923 TTTCCTCTTCAAGAAAGTAAAGAGTGGCAACTAAATACATCTCTTCTGTGTA 4982
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 2191
QY 4983 AAAGGAGAGATCTTAGGACTATTGGTCCAAATGGTCTGGCAAAAGCAATTTAAT 5042
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 2191
QY 5043 ATTCGTGGTGTGATATGCAACCACTTCAGGCCAGGTATTTTAGGAGATTTCTTCA 5102
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 2191
QY 5103 GAGCAAGTGAAGATGATGATCTACTGAAGTGTATGGTCTCTCTAGATAAACCTT 5162
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 2191
QY 5163 TTGTGGCCAGATCTACATTTGAGCAAGATTTTGAATTTATGAGAGTGTCAAGGATG 5222
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 2191
QY 5223 AGTCAAGTGAAGATGATGATCTACTGAAGTGTATGGTCTCTCTAGATAAACCTT 5162
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 2191
QY 5283 CATCTTCAGAGAGTGTAAAGAACTACTCTGAGAGATCAACCGAAAGTGTGTTTGTCT 5342
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 2191
QY 5343 CTAAGTATCTAGGAACTCTCAGATTTACTTTGTAGATGAACCATCTACAGGTATGAT 5402
Db TTTATTCATCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 2191

Db 2552 GCCTCTTGTCCACAAATCCCAAGGTTCTTTTATAGATGAGCCGACCATTTGGTGGAC 2611
QY 5403 CCCAAGCCAAACAGACACATGTCGGGAGCAATTCGAATCGCACTTTAAACACAGAAAGCGG 5462
Db 2612 GTTTCGGTTAAGGATNAATTCGTGGCAATTAATCTCAGATCAATCAAGAGGAAACT 2671
QY 5463 GCTGCTATTCTGACCACTCACTATATGAGGAGGAGGCTGTCTGTGATCGAGTAGCT 5522
Db 2672 ACCATTCTTTGACCACTCAGCATTTGAGTATATTGAGCACTTTGTCGATCGGATTTTC 2731
QY 5523 ATCATGCTGTCGGGAGTAAAGTATCGGAACAGTACACATCTAAAGAGTAAATTT 5582
Db 2732 ATGATTGACAGGGGCAAGAGATTTTGTGAAACGGTGAGCCAACTCAAGAGACCTTT 2791
QY 5583 GGAAA 5587
Db 2792 GGTAA 2796

RESULT 14

US-09-621-976-2582
; Sequence 2582, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2582
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 69..308
US-09-621-976-2582

Query Match 1.3%; Score 83.8; DB 4; Length 450;
Best Local Similarity 60.2%; Pred. No. 2.7e-10;
Matches 139; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
QY 5693 AAGTTTCTTCTATTTGGCTTATAAAATTCCTAAGGAAGATGTTCACTCCCTTTCACA 5752
Db 74 AAAATATTCTCTTTAATGGCGTATAAGTTACCTGTGGAGGATGCCACCCCTCTATCTCG 133
QY 5753 ATCTTTTTTAAGCTGGAAGAGCTAAACATCTTTTCCATTGAAGAATATAGCTTTTC 5812
Db 134 GGCTTTTCAAGTTAGAGCGCATGAACAGACCTTCAACCTGGAGGAATACAGCTCTC 193
QY 5813 TCAAGCAACATTGGAACAGGTTTGTAGAACTCACTAAAGAACAGAGGAGGAATAA 5872
Db 194 TCAGGCTACCTTGGAGCAGGTATCTTGAACCTCTGTAAGAGCAGGAGCTGGGAAATGT 253
QY 5873 TAGTTGTGAACTTTAAACAGCACACTTTGTGGGAAACGACACAGGAAGA 5923
Db 254 TGATGATAAAATTGATACAAACAGTTGAATGGAAACTTCTCCACAGGAAGA 304

RESULT 15

US-09-621-976-2581
; Sequence 2581, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2581
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 110..328
US-09-621-976-2581
Query Match 1.3%; Score 83.4; DB 4; Length 463;
Best Local Similarity 60.3%; Pred. No. 3.3e-10;
Matches 138; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 5695 GTTTTCTTCTATTTGGCTTATAAAATTCCTAAGGAAGATGTTCACTCCCTTTCACAAT 5754
Db 96 GATATTCTCTTTAATGGCGTATAAGTTACCTGTGGAGGATGCCACCTCTATCTCGGC 155
QY 5755 CTTTTTTTAAGCTGGAAGAGCTTAAACATGCTTTTGCCTATTGAAGAATATAGCTTTTCTC 5814
Db 156 CTTTTTCAAGTTAGAGGCGATGAAACAGACCTTCAACCTGGAGGAATACAGCCTCTCTC 215
QY 5815 AAGCAACATTGGAACAGGTTTGTAGAACTCACTAAAGAACAGAGGAGGAGATAATA 5874
Db 216 AGCTACCTTGGAGCAGGTATTCTTGAACCTCTGTAAGAGCAGGAGCTGGGAAATGTTG 275
QY 5875 GTTGTGGAACCTTTAAACAGCACACTTTGTGGGAAACGACACAAACAAGA 5923
Db 276 ATGATAAAATTGATACAAACAGTTGAATGGAAACTTCTCCACAGGAAGA 324

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Job time : 484 secs

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Sequence 37, Appl
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Sequence 16105, A
Sequence 16108, A

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18	1182	18.1	13346	15	US-10-171-581-333
19	1150.4	17.6	6181	14	US-10-005-338B-4
20	1118.8	17.1	5981	14	US-10-005-338B-3
21	1117.2	17.1	4875	13	US-10-090-454-3
22	1117.2	17.1	5018	13	US-10-090-454-1
23	1090.8	16.7	5296	14	US-10-005-338B-2
24	1089.2	16.7	5211	17	US-10-467-685-36
25	1086	16.6	4854	13	US-10-090-453A-3
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28	930.6	14.3	5149	15	US-10-343-903-60
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33	857.8	13.1	5622	18	US-10-343-903-42
34	797.4	12.2	5175	16	US-10-005-398-37
35	757.4	11.6	974	9	US-09-833-381-1085
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42	471.2	7.2	476	9	US-09-867-701-1362
43	459	7.0	465	16	US-10-242-353A-44227
44	459	7.0	465	16	US-10-085-783A-44227
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ALIGNMENTS

DEPT. 1

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US-10-005-338B-1
; Sequence 1, Application US/10005338B
; Publication No. US2003004895A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLÉ, Patrice
; APPLICANT: ROSIER-MONTUS, Marie-Francoise
; APPLICANT: FRADÉS, Catherine
; APPLICANT: ARNOULD-REGUIGNE, Isabelle
; APPLICANT: DUVERGER, Nicolas
; APPLICANT: ALLIKMETS, Rando
; APPLICANT: DEAN, Michael
; TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCAS, ABCA9, AND ABCA10
; FILE REFERENCE: ABCAS, 6, 9, 10
; CURRENT APPLICATION NUMBER: US/10/005,338B
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/263,231
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: FR 00403440.1
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO. 1
; LENGTH: 6525
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 4449
; OTHER INFORMATION: n=unknown, may be a o r g o r t
US-1-005-338B-1

Query Match 100.0%; Score 524; DB 14; Length 6525;
Best Local Similarity 100.0%; Pred. No. 0;

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Perfect score: 6525
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3694831 seqs, 2747406616 residues

Total number of hits satisfying chosen parameters: 7389662

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0$
                  Maximum Match 100%
                  Listing first 45 summaries

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Published Applications NA:*
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6: /cgn2_6/pdata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/pdata/2/pubpna/US08_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			Length	DB	ID	Description
	Score	Match					
1	6524	100.0	8525	14	US-10-005-338B-1		Sequence 1, Appli
2	6122.8	93.8	6369	18	US-10-343-903-33		Sequence 33, Appli
3	5373.2	82.3	5475	13	US-10-090-458-4		Sequence 4, Appli
4	5255.8	80.3	5463	13	US-10-090-458-1		Sequence 1, Appli
5	5247.4	80.4	5262	9	US-09-971-121-5		Sequence 5, Appli
6	4918.4	75.4	4929	9	US-09-971-121-1		Sequence 1, Appli
7	4807.4	73.7	4917	13	US-10-090-458-3		Sequence 3, Appli
8	4754.8	72.9	4785	9	US-09-971-121-3		Sequence 3, Appli
9	3258.2	49.9	3347	16	US-10-108-260A-160		Sequence 160, app
10	3178	48.7	3268	15	US-10-094-749-984		Sequence 984, App
11	1789.4	27.4	3328	10	US-09-822-846-98		Sequence 98, Appli
12	1731.8	26.5	1943	16	US-10-108-260A-1424		Sequence 1424, Ap

		Matches 6525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	AAAATGTTGATATTTCTCTTAGCAGGCTGTCACACAGGTTAGGTTACAGTCAATAAGTTT	60		
Db	1	AAAATGTTGATATTTCTCTTAGCAGGCTGTCACACAGGTTAGGTTACAGTCAATAAGTTT	60		
QY	61	CTACCACATCTTTGACGCTAGTGTTCATTTTAGTTTATTTTCAAAAACCTTTTGCG	120		
Db	61	CTACCACATCTTTGACGCTAGTGTTCATTTTAGTTTATTTTCAAAAACCTTTTGCG	120		
QY	121	TACCTTTTGGTCTGTCTTGTGTGTCCTTCAGTGAACAGTCTGGATTGGACAGTGGT	180		
Db	121	TACCTTTTGGTCTGTCTTGTGTGTCCTTCAGTGAACAGTCTGGATTGGACAGTGGT	180		
QY	181	CTGTCTGTAGTTCAGTTTCTCAAGCCTTGTGCACACTAATAGGATTGGATTATGTATG	240		
Db	181	CTGTCTGTAGTTCAGTTTCTCAAGCCTTGTGCACACTAATAGGATTGGATTATGTATG	240		
QY	241	TCCAGCTTGGGAATTAATACAGGAATTAATAACAACTTTTAGAGTGTCTTCCCTGAGCTC	300		
Db	241	TCCAGCTTGGGAATTAATACAGGAATTAATAACAACTTTTAGAGTGTCTTCCCTGAGCTC	300		
QY	301	TCCTTCTATTGTTGCCCTTCTACTTTTGTGCTTCCCTGTGGCTGTCTTCTATCTCC	360		
Db	301	TCCTTCTATTGTTGCCCTTCTACTTTTGTGCTTCCCTGTGGCTGTCTTCTATCTCC	360		
QY	361	AGCCAGAGAGCTAGTGTGTTTATTTCTCCATTGTGTTACACACTTGTGCGAGCTGCAACAC	420		
Db	361	AGCCAGAGAGCTAGTGTGTTTATTTCTCCATTGTGTTACACACTTGTGCGAGCTGCAACAC	420		
QY	421	CATATCCAGGCCCCAATGAGGTAGAGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	480		
Db	421	CATATCCAGGCCCCAATGAGGTAGAGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	480		
QY	481	TCCTTACACGATAGTTCATTTGAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	540		
Db	481	TCCTTACACGATAGTTCATTTGAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	540		
QY	541	GCACTAGGCTTTGTTACTGTAGTCTGCCCCTGTTTACCATGGGATTGCTTCATGTGGGG	600		
Db	541	GCACTAGGCTTTGTTACTGTAGTCTGCCCCTGTTTACCATGGGATTGCTTCATGTGGGG	600		
QY	601	ATACAGGAGATTCAG	660		
Db	601	ATACAGGAGATTCAG	660		
QY	661	AAGACTCTCCCTTGGCCATTCCTCAATTCAGAGCTAAGGCTTCTTCTGGAGCTGCTCTGT	720		
Db	661	AAGACTCTCCCTTGGCCATTCCTCAATTCAGAGCTAAGGCTTCTTCTGGAGCTGCTCTGT	720		
QY	721	GGGCGGTTGGGAGATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	780		
Db	721	GGGCGGTTGGGAGATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	780		
QY	781	ATTCTGTCTACCTTATTTACATGCTTGTGTTTCTTTTACAGAGCTGACAGATTGCTGCT	840		
Db	781	ATTCTGTCTACCTTATTTACATGCTTGTGTTTCTTTTACAGAGCTGACAGATTGCTGCT	840		
QY	841	CCATGCATCTCTCAGTTTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	900		
Db	841	CCATGCATCTCTCAGTTTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	900		
QY	901	CTGGGACTCAACAGCTGCTTATTTTGGCGTTTAAATAATCATGCAGTTTACTCGCTGGC	960		
Db	901	CTGGGACTCAACAGCTGCTTATTTTGGCGTTTAAATAATCATGCAGTTTACTCGCTGGC	960		
QY	961	TCCGGGTTTGTGTTTGTGTTTCTCTTAAATAGGTTTATTCAGAGAGAGAGAGAGAGAG	1020		
Db	961	TCCGGGTTTGTGTTTGTGTTTCTCTTAAATAGGTTTATTCAGAGAGAGAGAGAGAGAG	1020		
QY	1021	CAATTAGGAGGTAGGAGTTGGAGACAGACAGACAGACAGACAGACAGACAGACAGACAG	1080		
Db	1021	CAATTAGGAGGTAGGAGTTGGAGACAGACAGACAGACAGACAGACAGACAGACAGACAG	1080		

QY	1081	TTAAATGCAGAACCAAAAAGAGTAGTGTTCAGGAATTTCTTTTCCACTATTTTTTTAT	1140		
Db	1081	TTAAATGCAGAACCAAAAAGAGTAGTGTTCAGGAATTTCTTTTCCACTATTTTTTTAT	1140		
QY	1141	TTTGGTAAATATTAATTTAGCATGATGCATCCAAATAAGAGAAATATGAAGAAGTGCCTAATA	1200		
Db	1141	TTTGGTAAATATTAATTTAGCATGATGCATCCAAATAAGAGAAATATGAAGAAGTGCCTAATA	1200		
QY	1201	TAGAACTCAATCTCTATGGCAAGTTTACTCTTTCTTAATCTAATTTCTTGGATATCTCCAG	1260		
Db	1201	TAGAACTCAATCTCTATGGCAAGTTTACTCTTTCTTAATCTAATTTCTTGGATATCTCCAG	1260		
QY	1261	TGACTAATATTAACAAGCAGCATCATCAGAAAAGTGTACTCATCATCTACCTGATGTCA	1320		
Db	1261	TGACTAATATTAACAAGCAGCATCATCAGAAAAGTGTACTCATCATCTACCTGATGTCA	1320		
QY	1321	TAATTAAGAGAAATATACAAAATGAAAAAGAAATGTAAATCCAGTCTCTCTAAAGCGGA	1380		
Db	1321	TAATTAAGAGAAATATACAAAATGAAAAAGAAATGTAAATCCAGTCTCTCTAAAGCGGA	1380		
QY	1381	GCAACTTGTAGTGTGGTTTCAAGAGCTCCATGTCCTATGAATTCGTTTTTTTCTG	1440		
Db	1381	GCAACTTGTAGTGTGGTTTCAAGAGCTCCATGTCCTATGAATTCGTTTTTTTCTG	1440		
QY	1441	ATAATGATTCAGTATCTTCTATTTATATGATTCAGAGCTGGCTGTTCAAAATCATGTG	1500		
Db	1441	ATAATGATTCAGTATCTTCTATTTATATGATTCAGAGCTGGCTGTTCAAAATCATGTG	1500		
QY	1501	AGGCTCTCAGTACTGGTCTCAGGTTTCAAGTTTACAGATCCATAGATGTGCCA	1560		
Db	1501	AGGCTCTCAGTACTGGTCTCAGGTTTCAAGTTTACAGATCCATAGATGTGCCA	1560		
QY	1561	TTATACAGTTGAAGACCAATGTTCTCTTTGGAAGAGCTGGAGTCACTAAAGCTGTGA	1620		
Db	1561	TTATACAGTTGAAGACCAATGTTCTCTTTGGAAGAGCTGGAGTCACTAAAGCTGTGA	1620		
QY	1621	TTATGGAGAAATCTGCTGTGTAGAAAATAGATACCTTTCCCGAGGAGTAATTTTAAAT	1680		
Db	1621	TTATGGAGAAATCTGCTGTGTAGAAAATAGATACCTTTCCCGAGGAGTAATTTTAAAT	1680		
QY	1681	ACCTAGTTATAGCATTTTCCACCTTTTGGATATCTTTTGGCAATTCATATCGTAGAGAAA	1740		
Db	1681	ACCTAGTTATAGCATTTTCCACCTTTTGGATATCTTTTGGCAATTCATATCGTAGAGAAA	1740		
QY	1741	AAGAAAAAATAAAGAAATTTTAAAGATAATGGACTTCATGATCTGCTTTTGGC	1800		
Db	1741	AAGAAAAAATAAAGAAATTTTAAAGATAATGGACTTCATGATCTGCTTTTGGC	1800		
QY	1801	TTTCTCGGCTTCTCTATATACAGTTTAAATTTTCTTATGTCCTCTTATGGCAGTCA	1860		
Db	1801	TTTCTCGGCTTCTCTATATACAGTTTAAATTTTCTTATGTCCTCTTATGGCAGTCA	1860		
QY	1861	TTGCGACAGCTTCTTTGTTTATTTCCCTCAAAGTAGCAGCATTTGTGATTTCTGCTTTT	1920		
Db	1861	TTGCGACAGCTTCTTTGTTTATTTCCCTCAAAGTAGCAGCATTTGTGATTTCTGCTTTT	1920		
QY	1921	TCTTTTATGATATCATCTGTATTTTGTCTTAAATGCTGACACTCTTTTAAATAAT	1980		
Db	1921	TCTTTTATGATATCATCTGTATTTTGTCTTAAATGCTGACACTCTTTTAAATAAT	1980		
QY	1981	CAAAACATCTGGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATTTATGGCCCTTA	2040		
Db	1981	CAAAACATCTGGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATTTATGGCCCTTA	2040		
QY	2041	TGATAATCTCTATAGAAAGTTTCCAAATCTGTAGTGTGGCTTTTCTAGTCTTTCTGTC	2100		
Db	2041	TGATAATCTCTATAGAAAGTTTCCAAATCTGTAGTGTGGCTTTTCTAGTCTTTCTGTC	2100		
QY	2101	ACTGTACTTTTGTGATTTGGTATTTGCACAGGTTCATCATTTAGAAGATTTTAAATGAAGTG	2160		
Db	2101	ACTGTACTTTTGTGATTTGGTATTTGCACAGGTTCATCATTTAGAAGATTTTAAATGAAGTG	2160		

2161 QY CTTCAATTTTCAAATTTGACTGCGAGGCCATATCTCTTAATTATTACAATTTATCATGCTCA 2220
2161 Db CTTCAATTTTCAAATTTGACTGCGAGGCCATATCTCTTAATTATTACAATTTATCATGCTCA 2220
2221 QY CACTTAATAGTATATTTCTATCTCTTCTGCTCTCTATCTCTGATCAAGTCATTTCCAGGGG 2280
2221 Db CACTTAATAGTATATTTCTATCTCTTCTGCTCTCTATCTCTGATCAAGTCATTTCCAGGGG 2280
2281 QY AATTTGCTTTACGGAGATCATCTTTATATTTTCTGAGGCCCTTCATATTTGTCACAAAGTA 2340
2281 Db AATTTGCTTTACGGAGATCATCTTTATATTTTCTGAGGCCCTTCATATTTGTCACAAAGTA 2340
2341 QY AAGAAATTTATGAGGAGTTATCAGAGGCCAATGTTAATGGAATATTTAGTTTTAGTCAAA 2400
2341 Db AAGAAATTTATGAGGAGTTATCAGAGGCCAATGTTAATGGAATATTTAGTTTTAGTCAAA 2400
2401 QY TTATTGACCAAGTTCTTTCAGAAATTTGTAGRAAAGAGCCATAAGAAATAGTGGTATTC 2460
2401 Db TTATTGACCAAGTTCTTTCAGAAATTTGTAGRAAAGAGCCATAAGAAATAGTGGTATTC 2460
2461 QY AGAAGACATACAGAAAGAGGTTGAAATTTGAGGCTTTGAGAAATTTTGTCAATTTGACA 2520
2461 Db AGAAGACATACAGAAAGAGGTTGAAATTTGAGGCTTTGAGAAATTTTGTCAATTTGACA 2520
2521 QY TATATGAGGTCAGATTACTGCTTACTTGGCCACAGTGGACAGGAAAGAGTACATTGA 2580
2521 Db TATATGAGGTCAGATTACTGCTTACTTGGCCACAGTGGACAGGAAAGAGTACATTGA 2580
2581 QY TGAATATCTTTGTTGGACTCTGCCACCTTCTGATGGTTTGCATCTATATATGGACACA 2640
2581 Db TGAATATCTTTGTTGGACTCTGCCACCTTCTGATGGTTTGCATCTATATATGGACACA 2640
2641 QY GAGTCTCAGAAATAGATGAAATGTTGAAGCAAGAAAAAATGATGGCATTTGTCACAGT 2700
2641 Db GAGTCTCAGAAATAGATGAAATGTTGAAGCAAGAAAAAATGATGGCATTTGTCACAGT 2700
2701 QY TAGATATACATTTGATGTTTGGACGTAGAGAAATTTATCAATTTTGGCTTCAATCA 2760
2701 Db TAGATATACATTTGATGTTTGGACGTAGAGAAATTTATCAATTTTGGCTTCAATCA 2760
2761 QY AAGGGATACCAAGCAAAATATAACAAGAAAGTCAGAAAGTTTACTAGATTTAGACA 2820
2761 Db AAGGGATACCAAGCAAAATATAACAAGAAAGTCAGAAAGTTTACTAGATTTAGACA 2820
2821 QY TGCAGACTATCAAGATACCAAGCTAAAAATTAAGTGGTGGTCAAAAAAGAAAGCTGT 2880
2821 Db TGCAGACTATCAAGATACCAAGCTAAAAATTAAGTGGTGGTCAAAAAAGAAAGCTGT 2880
2881 QY CATTAGGAATGCTGTTCTTGGGAACCCAAAGATACCTGCTAGATGAAACCAACAGCTG 2940
2881 Db CATTAGGAATGCTGTTCTTGGGAACCCAAAGATACCTGCTAGATGAAACCAACAGCTG 2940
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2941 Db GAATGGACCCCTGTTCTCGACATATGTTATGGAATCTTTTAAAAATACAGAAAAAGCCAAATC 3000
3001 QY GGGTCAGAGTGTTCAGTACTCATTTCTAGTGGAGTGCATCTTTCAGATAGGAAG 3060
3001 Db GGGTCAGAGTGTTCAGTACTCATTTCTAGTGGAGTGCATCTTTCAGATAGGAAG 3060
3061 QY CTGTGATATCAAGAAATGCTGAAATGTTGTTGTTCTTCAATGTTCTCAAAAAGTAAAT 3120
3061 Db CTGTGATATCAAGAAATGCTGAAATGTTGTTGTTCTTCAATGTTCTCAAAAAGTAAAT 3120
3121 QY GGGGAATCGGCTACCGCTGAGCATGTATACATAGACAAATATTTGCCACAGAAATCTCTTT 3180
3121 Db GGGGAATCGGCTACCGCTGAGCATGTATACATAGACAAATATTTGCCACAGAAATCTCTTT 3180
3181 QY CTTCACTGTTTAAACAAATATACCTCGAGCTACTTTTATACACAGAAATGACCAACAAC 3240
3181 Db CTTCACTGTTTAAACAAATATACCTCGAGCTACTTTTATACACAGAAATGACCAACAAC 3240
3241 QY TTGTGTATAGCTTGCTTTTCAAGGACATGGACAAATTTTCAGGTTTGTGTTCTGCCCTAG 3300

3241 Db TTGTGTATAGCTTGCTTTTCAAGGACATGGACAAATTTTCAGGTTTGTGTTCTGCCCTAG 3300
3301 QY ACAGTCATTCAAATTTGGTGTCTATTCTTATGGTGTTCATGACAGCTTTTGAAGACG 3360
3301 Db ACAGTCATTCAAATTTGGTGTCTATTCTTATGGTGTTCATGACAGCTTTTGAAGACG 3360
3361 QY TATTTTTAAAGCTAGAAGTTGAAGCAGAAATTTGACCAAGCAGATTTATAGTGTATTCTC 3420
3361 Db TATTTTTAAAGCTAGAAGTTGAAGCAGAAATTTGACCAAGCAGATTTATAGTGTATTCTC 3420
3421 QY AGCAGCCACTGGAGGAAGAAATGGATTCAAATCTTTTGATGAAATGGAACAGAGCTTAC 3480
3421 Db AGCAGCCACTGGAGGAAGAAATGGATTCAAATCTTTTGATGAAATGGAACAGAGCTTAC 3480
3481 QY TTATTCTTTCTGAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGGAACCAACAGA 3540
3481 Db TTATTCTTTCTGAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGGAACCAACAGA 3540
3541 QY TGTATACAAATAGCAAAAGTTTCATTTCTTACCTTGAACGTTGAAAGTAAATCAGTGAGAT 3600
3541 Db TGTATACAAATAGCAAAAGTTTCATTTCTTACCTTGAACGTTGAAAGTAAATCAGTGAGAT 3600
3601 QY CAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTTGGTTCATC 3660
3601 Db CAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTTGGTTCATC 3660
3661 QY ACTCTTTTAAAAAATGCTGTGTTCCATCAAACTTGTTCAGACTTATATTTCTTAAAC 3720
3661 Db ACTCTTTTAAAAAATGCTGTGTTCCATCAAACTTGTTCAGACTTATATTTCTTAAAC 3720
3721 QY CTGGAGACAAACCATATAAATACAAACAAAGTCCTCTTCTTCAAAATTTCTGCTGACTCAG 3780
3721 Db CTGGAGACAAACCATATAAATACAAACAAAGTCCTCTTCTTCAAAATTTCTGCTGACTCAG 3780
3781 QY ATATCAGTGATCTTATTAGCTTTTTTCAACAGCAGAACATAATGTGACGATTAATG 3840
3781 Db ATATCAGTGATCTTATTAGCTTTTTTCAACAGCAGAACATAATGTGACGATTAATG 3840
3841 QY ACAGTGACTATGATTCGTTGGCTCCCCATAGTCGGCTTTAAATGTGATGCAATTCAGAAA 3900
3841 Db ACAGTGACTATGATTCGTTGGCTCCCCATAGTCGGCTTTAAATGTGATGCAATTCAGAAA 3900
3901 QY AGSACTATCTTTTTCAGCTGTTTTTCAACAGTACTATGTTTATTTCTTTACCTATATTAG 3960
3901 Db AGSACTATCTTTTTCAGCTGTTTTTCAACAGTACTATGTTTATTTCTTTACCTATATTAG 3960
3961 QY TGAATATCATTAAGTAACTACTATCTTTATCATTTAAATGTGACTGAAACCATCCAGATCT 4020
3961 Db TGAATATCATTAAGTAACTACTATCTTTATCATTTAAATGTGACTGAAACCATCCAGATCT 4020
4021 QY GGAGTACCCCATTTCTTCAAGAAATTAAGTATAGTTTTTAAAAATGAGCTGTTATTTTC 4080
4021 Db GGAGTACCCCATTTCTTCAAGAAATTAAGTATAGTTTTTAAAAATGAGCTGTTATTTTC 4080
4081 QY AAGCAGCTTTGCTTGGAAATCATTTGTTACTGCAATGCCACCTTACCTTGGCATGGAAAAATG 4140
4081 Db AAGCAGCTTTGCTTGGAAATCATTTGTTACTGCAATGCCACCTTACCTTGGCATGGAAAAATG 4140
4141 QY CAGAGAAATCATAGATCAAGCTTATCTCAACTTAACTTTTCAGCTTTTGGCATCTG 4200
4141 Db CAGAGAAATCATAGATCAAGCTTATCTCAACTTAACTTTTCAGCTTTTGGCATCTG 4200
4201 QY CATATTGGATTTGGACAAAGCTGTTTGTGATATCCCTTATTTTTTATCATTTCTTATTTGA 4260
4201 Db CATATTGGATTTGGACAAAGCTGTTTGTGATATCCCTTATTTTTTATCATTTCTTATTTGA 4260
4261 QY TGTAGGAAGCTTACTGGCATTTTATGATTTATTTTTTATCTGTAAGATTCCTTG 4320
4261 Db TGTAGGAAGCTTACTGGCATTTTATGATTTATTTTTTATCTGTAAGATTCCTTG 4320
4321 QY CTGCTGTTTCTGCTTTATGTTATGTTCCATCAGTATTCTGTTCACTTATATGCTT 4380

Db	4321	CTGTGGTTTTTGGCCTTATTGGTTATGTTCCATCAGTATATCTGTGTCACCTTATTTGCTTT	4380
Qy	4381	CTTTTCCACCTTTTAAAGAAAAATTTTAAATACCAAAGAAATTTTGGTCATTTATCTATTTCTGTGG	4440
Db	4381	CTTTTCCACCTTTTAAAGAAAAATTTTAAATACCAAAGAAATTTTGGTCATTTATCTATTTCTGTGG	4440
Qy	4441	CAGCGTTGNCCTTGTAITGCAATCAGTGAANATACTTCTTTATGGGATACACAATTTGCCA	4500
Db	4441	CAGCGTTGNCCTTGTAITGCAATCAGTGAANATACTTCTTTATGGGATACACAATTTGCCA	4500
Qy	4501	CTATTTCTTCATTTAGCCTTTTGTATCATCATTTCCAATCTATCCAATCTTCTAGGTGTCCTGA	4560
Db	4501	CTATTTCTTCATTTAGCCTTTTGTATCATCATTTCCAATCTATCCAATCTTCTAGGTGTCCTGA	4560
Qy	4561	TTTCTTTTCAATAAGATTTCTTTGGAGAATGTACGAAAAAATGTGGACACCTATAATATCCAT	4620
Db	4561	TTTCTTTTCAATAAGATTTCTTTGGAGAATGTACGAAAAAATGTGGACACCTATAATATCCAT	4620
Qy	4621	GGGATAGGCTTTTCAGTAGCTGTTTATATCGCCTTACCTGCACTGTGTACTGTGCAATTTCC	4680
Db	4621	GGGATAGGCTTTTCAGTAGCTGTTTATATCGCCTTACCTGCACTGTGTACTGTGCAATTTCC	4680
Qy	4681	TCTTACAATACTATGAGAAAAAATATGGAGCGAGATCAATAAGAAAAAGATTCCTTTTTCAT	4740
Db	4681	TCTTACAATACTATGAGAAAAAATATGGAGCGAGATCAATAAGAAAAAGATTCCTTTTTCAT	4740
Qy	4741	GAACCTTTTCAACGGAAGCTCTAATAATAGGAAGCTTCCAGAACCCACAGACAATGAGGATG	4800
Db	4741	GAACCTTTTCAACGGAAGCTCTAATAATAGGAAGCTTCCAGAACCCACAGACAATGAGGATG	4800
Qy	4801	AAGATGAAGATGTCAAAGCTCAAAGACTAAAGGTCAAAGAGCTGATGGGTGTCGACAGTGT	4860
Db	4801	AAGATGAAGATGTCAAAGCTCAAAGACTAAAGGTCAAAGAGCTGATGGGTGTCGACAGTGT	4860
Qy	4861	GTGAGHGAAACCATTCATTTATGGTCAGCAATTTGCAATAAGAAATATGATGACAAGAAAG	4920
Db	4861	GTGAGHGAAACCATTCATTTATGGTCAGCAATTTGCAATAAGAAATATGATGACAAGAAAG	4920
Qy	4921	ATTTTCTTCTTTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTGTGTGA	4980
Db	4921	ATTTTCTTCTTTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTGTGTGA	4980
Qy	4981	AAAAAGAGAGATCTTTAGGACTATTTGGGTCCAAATGGTGTGCGCAAAAGCACAATTTATTA	5040
Db	4981	AAAAAGAGAGATCTTTAGGACTATTTGGGTCCAAATGGTGTGCGCAAAAGCACAATTTATTA	5040
Qy	5041	ATATTTCTGGTTGTGATTTAAACCACTTTCAGCCAGGATTTTATAGGAGATTTATCTTT	5100
Db	5041	ATATTTCTGGTTGTGATTTAAACCACTTTCAGCCAGGATTTTATAGGAGATTTATCTTT	5100
Qy	5101	CAGAGACAAGTGAAGATGATTCATCTGAAGTGTATGGGTACTGTCTTCAGATAAAC	5160
Db	5101	CAGAGACAAGTGAAGATGATTCATCTGAAGTGTATGGGTACTGTCTTCAGATAAAC	5160
Qy	5161	CTTTTGTGCGCAGATACCTACATTTGAGGAAATTTTGAAGAAATTTATGGAGCTGTCAAGGAA	5220
Db	5161	CTTTTGTGCGCAGATACCTACATTTGAGGAAATTTTGAAGAAATTTATGGAGCTGTCAAGGAA	5220
Qy	5221	TGAGTCAAGTGCATCAAAAGAAAGTCAATAAGTCCAAATACACATGCATTTGATTTAAAG	5280
Db	5221	TGAGTCAAGTGCATCAAAAGAAAGTCAATAAGTCCAAATACACATGCATTTGATTTAAAG	5280
Qy	5281	AACATCTTCAGAGACTGTGTAAGAACTACTCGCAGGAATCAACGHAAGTTGTGTTTTG	5340
Db	5281	AACATCTTCAGAGACTGTGTAAGAACTACTCGCAGGAATCAACGHAAGTTGTGTTTTG	5340
Qy	5341	CTCTAAGTATGCTAGGGAATCCTCAGATTTACTTTGCTAGATGAACCATCTACAGGTATGG	5400
Db	5341	CTCTAAGTATGCTAGGGAATCCTCAGATTTACTTTGCTAGATGAACCATCTACAGGTATGG	5400
Qy	5401	ATCCCAAGCCAAACAGCAATGTGGCGAGCAATTCGAATGTGCAATTTAAAAACAGAAAGC	5460
Db	5401	ATCCCAAGCCAAACAGCAATGTGGCGAGCAATTCGAATGTGCAATTTAAAAACAGAAAGC	5460

Qy	5461	GGGCTGCTATTCTGACCACTTACTATATGAGAGAGCGAGGCGTGTCTGTGATCGAGTAG	5520
Db	5461	GGGCTGCTATTCTGACCACTTACTATATGAGAGAGCGAGGCGTGTCTGTGATCGAGTAG	5520
Qy	5521	CTATCATGTGTCTGGCGAGTTAAGATGTATCGGAACAGTACCAACTCTAAAGAGTAAAT	5580
Db	5521	CTATCATGTGTCTGGCGAGTTAAGATGTATCGGAACAGTACCAACTCTAAAGAGTAAAT	5580
Qy	5581	TTGGAAAAGGCTACTTTTTCGGAATTTAAATGAAGACTGGATAGAAAACCTTAGAGTAG	5640
Db	5581	TTGGAAAAGGCTACTTTTTCGGAATTTAAATGAAGACTGGATAGAAAACCTTAGAGTAG	5640
Qy	5641	ACGCCCTTCAAGAGAAATTCAGTATATTTTCCCAATGCAAGCCGTCAGGAAAAGTTTTT	5700
Db	5641	ACGCCCTTCAAGAGAAATTCAGTATATTTTCCCAATGCAAGCCGTCAGGAAAAGTTTTT	5700
Qy	5701	CTTCTATTTTGGCTTATAAAATTCCTAAGAAAGATGTTTCAGTCCCTTTCACAATCTTTTT	5760
Db	5701	CTTCTATTTTGGCTTATAAAATTCCTAAGAAAGATGTTTCAGTCCCTTTCACAATCTTTTT	5760
Qy	5761	TTAAGCTTGGAAAGCTTAAACATGCTTTTCCCATTTGAAGAAATATAGCTTTTCTCAAGCAA	5820
Db	5761	TTAAGCTTGGAAAGCTTAAACATGCTTTTCCCATTTGAAGAAATATAGCTTTTCTCAAGCAA	5820
Qy	5821	CATTGGAACAGGTTTTTGTAGAACTCACTAAAGAACAGAGGAGGAGATAATAGTTGTC	5880
Db	5821	CATTGGAACAGGTTTTTGTAGAACTCACTAAAGAACAGAGGAGGAGATAATAGTTGTC	5880
Qy	5881	GAACTTTTAAACAGCACACTTTGTGGGAAACGAAACACAAGAAAGATAGAGTAGTATTTTGA	5940
Db	5881	GAACTTTTAAACAGCACACTTTGTGGGAAACGAAACACAAGAAAGATAGAGTAGTATTTTGA	5940
Qy	5941	TTTGTATTTGTCGCTCTGCTTACTGGAGCTCTTTCTTTTCACTTAAATTTTAACTTTGG	6000
Db	5941	TTTGTATTTGTCGCTCTGCTTACTGGAGCTCTTTCTTTTCACTTAAATTTTAACTTTGG	6000
Qy	6001	TTTAAAAAGTTTTTTTATTTGAATTGGTAACTGAGAAACCAAGAACGCACTTGAATTTTTC	6060
Db	6001	TTTAAAAAGTTTTTTTATTTGAATTGGTAACTGAGAAACCAAGAACGCACTTGAATTTTTC	6060
Qy	6061	TAAGCTCCTTAAATGAAATGCTGTGTTGCTTTTCTTTTCACTTAAATTTTAAATAAAACGTAT	6120
Db	6061	TAAGCTCCTTAAATGAAATGCTGTGTTGCTTTTCTTTTCACTTAAATTTTAAATAAAACGTAT	6120
Qy	6121	GTATAATTAAGTGAAGCTGCATGTTTGTATTGAAGTATATTGAACATATATAGTTTGTATG	6180
Db	6121	GTATAATTAAGTGAAGCTGCATGTTTGTATTGAAGTATATTGAACATATATAGTTTGTATG	6180
Qy	6181	TCATCTTTTTTCCATTCAGAAACAGCTTCTGAAATTTGCTGATTTTAAAGGAATTTGTAAT	6240
Db	6181	TCATCTTTTTTCCATTCAGAAACAGCTTCTGAAATTTGCTGATTTTAAAGGAATTTGTAAT	6240
Qy	6241	AGATAGTTTTATTTTAACTTATCTTAAAGTTTATGCCATCTTCTTAAATAAGTAGCTGA	6300
Db	6241	AGATAGTTTTATTTTAACTTATCTTAAAGTTTATGCCATCTTCTTAAATAAGTAGCTGA	6300
Qy	6301	ATGTTTCCAACTTAAATAAAACCTAATACATACTAATGATGATAAGAAAGATACATAAAGC	6360
Db	6301	ATGTTTCCAACTTAAATAAAACCTAATACATACTAATGATGATAAGAAAGATACATAAAGC	6360
Qy	6361	AATGTGAAGTTTTCTCTCTCTCTTTTAAATTTCTAAAAAGCCACTTTTGAATTTGGAAGT	6420
Db	6361	AATGTGAAGTTTTCTCTCTCTCTTTTAAATTTCTAAAAAGCCACTTTTGAATTTGGAAGT	6420
Qy	6421	TGTCATCCGTAAAGCTGGAAGTGTGAAGCACTAGAGAAATCTCAATATAGAGATTTTGAGAA	6480
Db	6421	TGTCATCCGTAAAGCTGGAAGTGTGAAGCACTAGAGAAATCTCAATATAGAGATTTTGAGAA	6480
Qy	6481	AGTTTATATCCACTAGGTGGCAGCTCATTTGATCATTAATTAAGTGAAT	6525
Db	6481	AGTTTATATCACTAGGTGGCAGCTCATTTGATCATTAATTAAGTGAAT	6525

RESULT 2

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; Sequence 33, Application US/10343903
; Publication No. US20040224911A1
; GENERAL INFORMATION:
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; APPLICANT: THORNTON, Michael; RAMKUMAR, Jayalaxmi;
; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda;
; APPLICANT: BAUGHN, Mariah R.; YANG, Junning;
; APPLICANT: YAO, Monique G.; LAL, Preeti G.;
; APPLICANT: CHAWLA, Narinder K.; GANDHI, Ameena R.;
; APPLICANT: HAPALIA, April J.A.; NGUYEN, Damiel B.;
; APPLICANT: ASVIZU, Chandra S.; ELLIOTT, Vicki S.;
; APPLICANT: TRIBOULEY, Catherine M.; LU, Dyung Aina M.;
; APPLICANT: XU, Yuning; REDDI, Roopa;
; APPLICANT: HERNANDEZ, Roberto; BOROWSKY, Mark L.;
; APPLICANT: LO, Terence P.; LU, Yan;
; APPLICANT: POLICKY, Jennifer L.; GREENE, Barrie D.;
; APPLICANT: SANJAYWALA, Madhusudan M.; RAUMANN, Brigitte E.;
; APPLICANT: BUFORD, Neil; ISON, Craig H.;
; APPLICANT: LEE, Brinestine A.; DING, Li;
; APPLICANT: DAS, Debopriya; KALLICK, Deborah A.;
; APPLICANT: KHAN, Farrah A.; SEILHAWER, Jeffrey J.;
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0183 USN
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; PRIOR FILING DATE: 2000-08-18
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; PRIOR FILING DATE: 2000-08-10
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; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 6369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2798241CB1
US-10-343-903-33

Query Match 93.8%; Score 6122.8; DB 18; Length 6369;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6127; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 AAAATGTTGATATTTCTTAGCAGGCTGTCACACAGGTAGGTTGAGTTCATAGTTT 60
DB 228 AAAATGTTGATATTTCTTAGCAGGCTGTCACACAGGTAGGTTGAGTTCATAGTTT 287
QY 61 CTACCCACATCTTTGAACTGAGTTCATTTAGTTTATTTTCAAAAACCTTTTGCGAG 120
DB 288 CTACCCACATCTTTGAACTGAGTTCATTTAGTTTATTTTCAAAAACCTTTTGCGAG 347
QY 121 TACCTTTTGGTCTCTGTGTGTCCTTGCAGTGAACAGCTGGAATTCGACAGTGGT 180
DB 348 TACCTTTTGGTCTCTGTGTGTCCTTGCAGTGAACAGCTGGAATTCGACAGTGGT 407
QY 181 CTGTCTGTAGTTCAGTTCCTCAAGCCTTGTCACTAATAGGATTCGATTTATGTATG 240
DB 408 CTGTCTGTAGTTCAGTTCCTCAAGCCTTGTCACTAATAGGATTCGATTTATGTATG 467

QY 241 TCCAGCTTGGGAATTTATTACAGGAATTAATAAACAACTTTTATAGAGTGTCTTCTGAGCTC 300
DB TCCAGCTTGGGAATTTATTACAGGAATTAATAAACAACTTTTATAGAGTGTCTTCTGAGCTC 527
QY 301 TCTTTCTATTTGTTCCCTCTTCTACTTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB TCTTTCTATTTGTTCCCTCTTCTACTTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 587
QY 361 AGCCAGAGAGCTAGTGTGTTTATTTCTCCATTTGTGTATACACATTTGTGAGCTGCAACAC 420
DB AGCCAGAGAGCTAGTGTGTTTATTTCTCCATTTGTGTATACACATTTGTGAGCTGCAACAC 647
QY 421 CATATCCAGGGCCCAATGGTAGGAGGTAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 480
DB CATATCCAGGGCCCAATGGTAGGAGGTAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 707
QY 481 TCTTTACACAGATAGTTCATTTGAATAGAGAGAAAGGTTTCTCTGCTCAGAGTGTGCT 540
DB TCTTTACACAGATAGTTCATTTGAATAGAGAGAAAGGTTTCTCTGCTCAGAGTGTGCT 767
QY 541 GCATAGGCTTTTGTACTGTAGTCTGCCCTGTTTACATGGGATTTGCTGATGTTGGGG 600
DB GCATAGGCTTTTGTACTGTAGTCTGCCCTGTTTACATGGGATTTGCTGATGTTGGGG 827
QY 601 ATACAGGAGAAATTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 660
DB ATACAGGAGAAATTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 887
QY 661 AAGACCTCCCTTTGCCCATTTCTCAATTCAAAGCTAAGGCTTTCTCTGAGGTGCTCTGT 720
DB AAGACCTCCCTTTGCCCATTTCTCAATTCAAAGCTAAGGCTTTCTCTGAGGTGCTCTGT 947
QY 721 GGGCGGTTTCGGGAGATACCAAGGAGAAAGAAAGTACACATTTGATATGTTGTTATTTCAA 780
DB GGGCGGTTTCGGGAGATACCAAGGAGAAAGAAAGTACACATTTGATATGTTGTTATTTCAA 1007
QY 781 ATTCTGCTACCTATTTTCACATGCTTTGTTTACTTTTTCAGAGCTGACAGATTCGTCT 840
DB ATTCTGCTACCTATTTTCACATGCTTTGTTTACTTTTTCAGAGCTGACAGATTCGTCT 1067
QY 841 CCATGCATTTCTGCCAGTTTCTTAAGAGAGACAGCTTGGAGTATGCTTAATCCATCTTAC 900
DB CCATGCATTTCTGCCAGTTTCTTAAGAGAGACAGCTTGGAGTATGCTTAATCCATCTTAC 1127
QY 901 CTGGGACTGAAACAGCTGTTATTTGCGGTTTAAAAATTTACATGAGTTTACTGCTGCTGC 960
DB CTGGGACTGAAACAGCTGTTATTTGCGGTTTAAAAATTTACATGAGTTTACTGCTGCTGC 1187
QY 961 TCCGGGTTTGTGTTTGTGTTTTCCTCTTTAATAGTTTATTCAGAAACATGCTCACATG 1020
DB TCCGGGTTTGTGTTTGTGTTTTCCTCTTTAATAGTTTATTCAGAAACATGCTCACATG 1247
QY 1021 CAATTAGGAGGTAGGAGTTTGGAGACAGACACACTTCTACTGAGAAATTAATCTTAA 1080
DB CAATTAGGAGGTAGGAGTTTGGAGACAGACACACTTCTACTGAGAAATTAATCTTAA 1307
QY 1081 TTAATATGAGAACCAAAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACATTTTTTTTAT 1140
DB TTAATATGAGAACCAAAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACATTTTTTTTAT 1367
QY 1141 TTTGGTAAATATTAATTAGCATGATCCAAATAGAAATATAGAAAGTGCCTTAATA 1200
DB TTTGGTAAATATTAATTAGCATGATCCAAATAGAAATATAGAAAGTGCCTTAATA 1427
QY 1201 TAGAATCTAATCTTATGGACAAGTTTACTCTTTCTAATCTAATCTTCTGATATATCTCCAG 1260
DB TAGAATCTAATCTTATGGACAAGTTTACTCTTTCTAATCTAATCTTCTGATATATCTCCAG 1487
QY 1261 TGACTAATATTAACAGCAGCATCATCAGAAAGTGTCTACTGATCATCTACCTGATGTCA 1320
DB TGACTAATATTAACAGCAGCATCATCAGAAAGTGTCTACTGATCATCTACCTGATGTCA 1547
QY 1321 TAATTACTGAGAAATATACAAATGAAAGAAATGTTTAACATCCAGTCTCTCTAAGCCGA 1380

Db ||||| 1548 TAATTAAGAGAAATATACAAATGAAAAAGAAATGTTAAATCCAGTCTCTCTAAGCCGA 1607
QY ||||| 1381 GCAACTTTGTAGTGTGGTGTTCCTCAAGAGCTCCATGCTCTATGAATCTGGTGTTCCTG 1440
Db ||||| 1608 GCAACTTTGTAGTGTGGTGTTCCTCAAGAGCTCCATGCTCTATGAATCTGGTGTTCCTG 1667
QY ||||| 1441 ATATGATTCAGATATCTCTATTTATATGATTCAGAGCTGGCTGTTCAAAATCATGTG 1500
Db ||||| 1668 ATATGATTCAGATATCTCTATTTATATGATTCAGAGCTGGCTGTTCAAAATCATGTG 1727
QY ||||| 1501 AGCTCTCAGTACTGGTCTCCTCAGGTTTCAACAGTTTACAGCATCCATAGATGCTGCA 1560
Db ||||| 1728 AGCTCTCAGTACTGGTCTCCTCAGGTTTCAACAGTTTACAGCATCCATAGATGCTGCA 1787
QY ||||| 1561 TTATACAGTTGAGACCAATGTTTCTTTTGAAGAGCTGGAGTCAACTAAAGCTGTTA 1620
Db ||||| 1788 TTATACAGTTGAGACCAATGTTTCTTTTGAAGAGCTGGAGTCAACTAAAGCTGTTA 1847
QY ||||| 1621 TTATGGGAGAACTGCTGTGTAGAAATAGATACCTTTCCCGAGAGTAAATTTAATAT 1680
Db ||||| 1848 TTATGGGAGAACTGCTGTGTAGAAATAGATACCTTTCCCGAGAGTAAATTTAATAT 1907
QY ||||| 1681 ACCTAGTTATAGCATTTTCCACTTTTGGATACCTTTTGGCAATTCATATCGTAGCAGAAA 1740
Db ||||| 1908 ACCTAGTTATAGCATTTTCCACTTTTGGATACCTTTTGGCAATTCATATCGTAGCAGAAA 1967
QY ||||| 1741 AAAAAAATAAAGAAATTTTAAAGATTAATGGACTTCATGATCGCTTTGGC 1800
Db ||||| 1968 AAAAAAATAAAGAAATTTTAAAGATTAATGGACTTCATGATCGCTTTGGC 2027
QY ||||| 1801 TTTCCTGGGTCTCTATATACAAAGTTTAAATTTTCTTATGTCCTTCTTATGGCAGTCA 1860
Db ||||| 2028 TTTCCTGGGTCTCTATATACAAAGTTTAAATTTTCTTATGTCCTTCTTATGGCAGTCA 2087
QY ||||| 1861 TTGGCAGACGCTCTTTGTTTATTTCTCCTCAAGTAGCAGCATTTGATATTTCTGCTTTT 1920
Db ||||| 2088 TTGGCAGACGCTCTTTGTTTATTTCTCCTCAAGTAGCAGCATTTGATATTTCTGCTTTT 2147
QY ||||| 1921 TCCTTTATGATTAATCATCTGATTTTCTTAAATGCTGACCTCTTTTAAATAAAT 1980
Db ||||| 2148 TCCTTTATGATTAATCATCTGATTTTCTTAAATGCTGACCTCTTTTAAATAAAT 2207
QY ||||| 1981 CAAACATGTGGAAATGATTTGTTTGTACTGTGCTTTTGGATTTATGSCCTTA 2040
Db ||||| 2208 CAAACATGTGGAAATGATTTGTTTGTACTGTGCTTTTGGATTTATGSCCTTA 2267
QY ||||| 2041 TGATATCTCTATAGAACTTTTCCAAATCGTTAGTGTGGCTTTTCAGTCTTTCTGTC 2100
Db ||||| 2268 TGATATCTCTATAGAACTTTTCCAAATCGTTAGTGTGGCTTTTCAGTCTTTCTGTC 2327
QY ||||| 2101 ACTGTACTTTTGTGATTTGATTTGACAGCTCATGCAATTTAGAATTTTAAAGAGTG 2160
Db ||||| 2328 ACTGTACTTTTGTGATTTGATTTGACAGCTCATGCAATTTAGAATTTTAAAGAGTG 2387
QY ||||| 2161 CTTTCAATTTCAAAATTTGATCGAGGCCATATCTCTAATTAATTAATATCATGCTCA 2220
Db ||||| 2388 CTTTCAATTTCAAAATTTGATCGAGGCCATATCTCTAATTAATTAATATCATGCTCA 2447
QY ||||| 2221 CACTTAATAGTATATTTCTATGTCCTCTGGCTGTCTATCTGATCAAGTCAATCCAGGG 2280
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QY ||||| 2281 AATTGGCTTACGGAGATCATCTTTATATTTCTGAAGCTTCATATTTGGTCAAGAGTA 2340
Db ||||| 2508 AATTGGCTTACGGAGATCATCTTTATATTTCTGAAGCTTCATATTTGGTCAAGAGTA 2567
QY ||||| 2341 AAAAAATTTACGGAGTTTATCAGAGGCAATTTTAAATGGAATATTTAGTTTGTGAAA 2400
Db ||||| 2568 AAAAAATTTACGGAGTTTATCAGAGGCAATTTTAAATGGAATATTTAGTTTGTGAAA 2627
QY ||||| 2401 TTATTGAGCCAGTTCTTCTCAGAAATTTAGGAAAAAGAACCCATAGAAATAGTGATTC 2460

Db ||||| 2628 TTATTGAGCCAGTTTCTTCTCAGAAATTTGTAGAAAAAGAACCCATAGAAATAGTGATTC 2687
QY ||||| 2461 AGAAGACATACAGAAAGAGGGTGAATAATGTGAGGCTTTGAGAAATTTGTCTATTGACA 2520
Db ||||| 2688 AGAAGACATACAGAAAGAGGGTGAATAATGTGAGGCTTTGAGAAATTTGTCTATTGACA 2747
QY ||||| 2521 TATATGAGGCTCAGATTTACTGCTTCTCTGGCCACAGTGGAAACAGGAAAGATGACATTGA 2580
Db ||||| 2748 TATATGAGGCTCAGATTTACTGCTTCTCTGGCCACAGTGGAAACAGGAAAGATGACATTGA 2807
QY ||||| 2581 TGAATATTTCTTTGTGACTCTGCCACCTTCTGATCGGTTTGCATATATATGAGCACA 2640
Db ||||| 2808 TGAATATTTCTTTGTGACTCTGCCACCTTCTGATCGGTTTGCATATATATGAGCACA 2867
QY ||||| 2641 GAGTCTCAGAAATAGATGAATGTTTGAAGCAGAAATAATGATTGGCATTTGTCCACAGT 2700
Db ||||| 2868 GAGTCTCAGAAATAGATGAATGTTTGAAGCAGAAATAATGATTGGCATTTGTCCACAGT 2927
QY ||||| 2701 TAGATATACACTTTGATGTTTTCAGCAGTAGAAGAAATTTATCAATTTTGGCTTCAATCA 2760
Db ||||| 2928 TAGATATACACTTTGATGTTTTCAGCAGTAGAAGAAATTTATCAATTTTGGCTTCAATCA 2987
QY ||||| 2761 AAGGATACAGCCAAATATATATACAGAGTGCAGAGGTTTACTAGATTAGACA 2820
Db ||||| 2988 AAGGATACAGCCAAATATATATACAGAGTGCAGAGGTTTACTAGATTAGACA 3047
QY ||||| 2821 TGCAACTATCAAGATTAACCAAGCTTAAATAATTAAGTGGTCAAAAAGAAAGCTGT 2880
Db ||||| 3048 TGCAACTATCAAGATTAACCAAGCTTAAATAATTAAGTGGTCAAAAAGAAAGCTGT 3107
QY ||||| 2881 CATTAGAATGCTGTTCTTGGGAAACCAAGATACCTGCTAGATGAACCAAGCTG 2940
Db ||||| 3108 CATTAGAATGCTGTTCTTGGGAAACCAAGATACCTGCTAGATGAACCAAGCTG 3167
QY ||||| 2941 GAATGAGCCCTCTCTCGACATATTTGTAATGTAATCTTTTAAATACAGAAAGCCAAATC 3000
Db ||||| 3168 GAATGAGCCCTCTCTCGACATATTTGTAATGTAATCTTTTAAATACAGAAAGCCAAATC 3227
QY ||||| 3001 GGGTGACAGTGTTCAGTACTCTTTCATGATGAAGTGCATTTTGCAGATGAGAAAG 3060
Db ||||| 3228 GGGTGACAGTGTTCAGTACTCTTTCATGATGAAGTGCATTTTGCAGATGAGAAAG 3287
QY ||||| 3061 CTGTATATACAGAGATGCTGAATGTTGGTCTTCAATGTTCTCCTCAAGTAAAT 3120
Db ||||| 3288 CTGTATATACAGAGATGCTGAATGTTGGTCTTCAATGTTCTCCTCAAGTAAAT 3347
QY ||||| 3121 GGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTTGTCACAGATCTCTTT 3180
Db ||||| 3348 GGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTTGTCACAGATCTCTTT 3407
QY ||||| 3181 CTTCACTGTTTAAACAAATATACCTGGAGTACTTTTNTTAAAGATGACCAACAC 3240
Db ||||| 3408 CTTCACTGTTTAAACAAATATACCTGGAGTACTTTTNTTAAAGATGACCAACAC 3467
QY ||||| 3241 TTGTGTATAGCTTGCCTTTTCAAGGACATGACAAATTTTTCAGTTTGTCTTCCCTAG 3300
Db ||||| 3468 TTGTGTATAGCTTGCCTTTTCAAGGACATGACAAATTTTTCAGTTTGTCTTCCCTAG 3527
QY ||||| 3301 ACAGTCATTTCAAAATTTGGGTGTCATTTCTTATGGTGTTCATGACGATTTGGAAGAG 3360
Db ||||| 3528 ACAGTCATTTCAAAATTTGGGTGTCATTTCTTATGGTGTTCATGACGATTTGGAAGAG 3587
QY ||||| 3361 TATTTTAAAGCTAGAGTTGAGAGAAATGACCAAGCAGATTAATAGTATTTTACTC 3420
Db ||||| 3588 TATTTTAAAGCTAGAGTTGAGAGAAATGACCAAGCAGATTAATAGTATTTTACTC 3647
QY ||||| 3421 AGCAGCCACTGGAGGAAATGGAATCTTTTGTGAAATGGAACAGAGCTTAC 3480
Db ||||| 3648 AGCAGCCACTGGAGGAAATGGAATCTTTTGTGAAATGGAACAGAGCTTAC 3707
QY ||||| 3481 TTATTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCAGATGAGCTTTGGAACACAG 3540
Db ||||| 3708 TTATTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCAGATGAGCTTTGGAACACAG 3767

QY	3541	TGATACAAATAGCAAAAGTTTCATTTCTTTACCTTGAAACGCTGAAAGTAATCAGTGAGAT	3600	QY	4621	GGGATAGGCTTTTCAGTAGCTGTTATATATCGCTTACCTGCGAGTGTGTACTGTGGATTTTCC	4680
Db	3768	TGATACAAATAGCAAAAGTTTCATTTCTTTACCTTGAAACGCTGAAAGTAATCAGTGAGAT	3827	Db	4848	GGGATAGGCTTTTCAGTAGCTGTTATATATCGCTTACCTGCGAGTGTGTACTGTGGATTTTCC	4907
QY	3601	CAGTGTTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTTTGGTTTCATC	3660	QY	4681	TCTTACAAATCTATGAGAAAATATATGAGGCGAGATCAATTAAGAAAAGATCCCTTTTTC	4740
Db	3828	CAGTGTTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTTTGGTTTCATC	3887	Db	4908	TCTTACAAATCTATGAGAAAATATATGAGGCGAGATCAATTAAGAAAAGATCCCTTTTTC	4967
QY	3661	ACTCTTTTAAATATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATATTTTCTAAAC	3720	QY	4741	GAACCTTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCACAGACAATGAGGATG	4800
Db	3888	ACTCTTTTAAATATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATATTTTCTAAAC	3947	Db	4968	GAACCTTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCACAGACAATGAGGATG	5027
QY	3721	CTGAGAGCAAAACACATATAACAAACAGTCTGCTTCTCAAAATTTCTGCTGACTCAG	3780	QY	4801	AAGATGAAGATGTCAAAAGCTGAAAGACTTAAAGGTCCTGAAAGCTGATGGTTGCCAGTGT	4860
Db	3948	CTGAGAGCAAAACACATATAACAAACAGTCTGCTTCTCAAAATTTCTGCTGACTCAG	4007	Db	5028	AAGATGAAGATGTCAAAAGCTGAAAGACTTAAAGGTCCTGAAAGCTGATGGTTGCCAGTGT	5087
QY	3781	ATATCAGTGATCTTATTAGCTTTTTCACAAGCCAGAACATAAATGGTGACGATGATTAATG	3840	QY	4861	GTGAGGAGAAACCATCCATTTATGCTCAGCAATTTTGCATATAAGAAATATGATGACAAGAAAG	4920
Db	4008	ATATCAGTGATCTTATTAGCTTTTTCACAAGCCAGAACATAAATGGTGACGATGATTAATG	4067	Db	5088	GTGAGGAGAAACCATCCATTTATGCTCAGCAATTTTGCATATAAGAAATATGATGACAAGAAAG	5147
QY	3841	ACAGTACTATGATACCGTGGCTCCCATATGATGGGCTTTAAATGTGATGCATTCAGAA	3900	QY	4921	ATTTTCTTCTTCTCAAGAAAAGTAAAGAAAGTGGCAACTTAAATATACATCTCTTCTGTGTGA	4980
Db	4068	ACAGTACTATGATACCGTGGCTCCCATATGATGGGCTTTAAATGTGATGCATTCAGAA	4127	Db	5148	ATTTTCTTCTTCTCAAGAAAAGTAAAGAAAGTGGCAACTTAAATATACATCTCTTCTGTGTGA	5207
QY	3901	AGGACTATGTTTTGACAGCTGTTTTCAACAGTACTATGGTTTATCTTTACCTATATTAG	3960	QY	4981	AAAAAGGAGAGATCTTAGGACTTATTTGGTCCAAATGGTCTGGCAAAAGACCAATTATTA	5040
Db	4128	AGGACTATGTTTTGACAGCTGTTTTCAACAGTACTATGGTTTATCTTTACCTATATTAG	4187	Db	5208	AAAAAGGAGAGATCTTAGGACTTATTTGGTCCAAATGGTCTGGCAAAAGACCAATTATTA	5267
QY	3961	TGAATATCATTPAGTAACCTATCTTATCATTTAAATGTGACTGAAACCATCCAGATCT	4020	QY	5041	ATATTCTGTTGTCATATTGAACCAACTTCAGGCCAGGTATTTTATAGGAGATTTATCTT	5100
Db	4188	TGAATATCATTPAGTAACCTATCTTATCATTTAAATGTGACTGAAACCATCCAGATCT	4247	Db	5268	ATATTCTGTTGTCATATTGAACCAACTTCAGGCCAGGTATTTTATAGGAGATTTATCTT	5327
QY	4021	GGAGTACCCATCTTTCAAGAAATTTACTGATAGTTTTTAAATTTGAGCTGTATTTTC	4080	QY	5101	CAGAGACAAGTGAAGATGATGATTTCACTGAAGTGTATGGTTTACTGTCTCAGATAAAC	5160
Db	4248	GGAGTACCCATCTTTCAAGAAATTTACTGATAGTTTTTAAATTTGAGCTGTATTTTC	4307	Db	5328	CAGAGACAAGTGAAGATGATGATTTCACTGAAGTGTATGGTTTACTGTCTCAGATAAAC	5387
QY	4081	AAGCAGCTTTGCTTGGAAATCATTTCTTACTGCAATGCCACCTTACTTTGCCATGAAAATG	4140	QY	5161	CTTTGTCGCCAGATCTACATTTGCGAGGAACATTTTTGAAATTTATGAGCTGTCAAGGAA	5220
Db	4308	AAGCAGCTTTGCTTGGAAATCATTTCTTACTGCAATGCCACCTTACTTTGCCATGAAAATG	4367	Db	5388	CTTTGTCGCCAGATCTACATTTGCGAGGAACATTTTTGAAATTTATGAGCTGTCAAGGAA	5447
QY	4141	CAGAGATCATTAAGATCAAGCTTATCTCAACTTAACTTTCAAGTCTTTTGGCCATCTG	4200	QY	5221	TGAGTGCAGTGAACATGAAAGAAAGTCATAAGTTCGAATTAACATCATCTGATTTTAAAG	5280
Db	4368	CAGAGATCATTAAGATCAAGCTTATCTCAACTTAACTTTCAAGTCTTTTGGCCATCTG	4427	Db	5448	TGAGTGCAGTGAACATGAAAGAAAGTCATAAGTTCGAATTAACATCATCTGATTTTAAAG	5507
QY	4201	CATATTGATTTGGACAGCTGTTGTGATATCCCTTATTTTATCATTTCTTATTTTGA	4260	QY	5281	AAACATCTTCAGAAAGCTGTAAAGAAATCTCTGCGAGGAATCAACGAAAGTTGTCTTTG	5340
Db	4428	CATATTGATTTGGACAGCTGTTGTGATATCCCTTATTTTATCATTTCTTATTTTGA	4487	Db	5508	AAACATCTTCAGAAAGCTGTAAAGAAATCTCTGCGAGGAATCAACGAAAGTTGTCTTTG	5567
QY	4261	TGCTAGGAAGCTTACTGSCATTTTCAATATGGAATATATTTTATCTGTAAGATTCCTTG	4320	QY	5341	CTCTAAGTATGCTAGGGAATCCTCAGATTTACTTTGCTAGATGAACCATCTACAGGTATGG	5400
Db	4488	TGCTAGGAAGCTTACTGSCATTTTCAATATGGAATATATTTTATCTGTAAGATTCCTTG	4547	Db	5568	CTCTAAGTATGCTAGGGAATCCTCAGATTTACTTTGCTAGATGAACCATCTACAGGTATGG	5627
QY	4321	CTGTGGTTTTTGGCTTATGTTATGTTTCCATCAGTTATCTGTTCACTTATATTTGCTT	4380	QY	5401	ATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAATCTGCATTTAAAAACAGAAAGC	5460
Db	4548	CTGTGGTTTTTGGCTTATGTTATGTTTCCATCAGTTATCTGTTCACTTATATTTGCTT	4607	Db	5628	ATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAATCTGCATTTAAAAACAGAAAGC	5687
QY	4381	CTTTCACTTTTAAAGAAAATTTTAAATACCAAGAAATTTTGGTCAATTTATCTATCTG	4440	QY	5461	GGGCTGCTATCTGACCACTCTACTATATGAGGAGGAGGAGGCTGTCTGTATCCAGTAG	5520
Db	4608	CTTTCACTTTTAAAGAAAATTTTAAATACCAAGAAATTTTGGTCAATTTATCTATCTG	4667	Db	5688	GGGCTGCTATCTGACCACTCTACTATATGAGGAGGAGGAGGCTGTCTGTATCCAGTAG	5747
QY	4441	CAGCTTGNCTGTGATTCGAATCACTGAATAACTTTTCTTTATGGGATACACAAATGCAA	4500	QY	5521	CTATCATGTGTCTGCGCAGTTTAAAGATGTATCGGAACAGTACAACATCTTAAAGAGTAAAT	5580
Db	4668	CAGCTTGNCTGTGATTCGAATCACTGAATAACTTTTCTTTATGGGATACACAAATGCAA	4727	Db	5748	CTATCATGTGTCTGCGCAGTTTAAAGATGTATCGGAACAGTACAACATCTTAAAGAGTAAAT	5807
QY	4501	CTATTCTTCATATATGCTTTTGTATCATCTATCCAAATCTATCCACTCTAGGTGGCTGA	4560	QY	5581	TTGGAAAAGGCTTACTTTTTTGGAAAATTTAAATTTGAAGACTGGATAGAAAACCTTAGAAGTAG	5640
Db	4728	CTATTCTTCATATATGCTTTTGTATCATCTATCCAAATCTATCCACTCTAGGTGGCTGA	4787	Db	5808	TTGGAAAAGGCTTACTTTTTTGGAAAATTTAAATTTGAAGACTGGATAGAAAACCTTAGAAGTAG	5867
QY	4561	TTTCTTTTCAAAAGATTTCTTGGAAAGATGTACGAAAAAATGTGGACACCTTATATTCAT	4620	QY	5641	ACCGCTTCAAAAGAGAAAATTCAGTATATTTTCCAAAATGCAAGCCGTTCAGGAAAGTTTTT	5700
Db	4788	TTTCTTTTCAAAAGATTTCTTGGAAAGATGTACGAAAAAATGTGGACACCTTATATTCAT	4847	Db	5868	ACCGCTTCAAAAGAGAAAATTCAGTATATTTTCCAAAATGCAAGCCGTTCAGGAAAGTTTTT	5927
				QY	5701	CTTCTATTTTGGGCTTATAAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTTCAATCTTTTT	5760

Db 1357 TCTATCTTGATCAAGTCATTCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 1416
Qy 2314 TGAAGCCTTCATATTTGGTCAAGAGCTAAAGAAATTTATGAGNGTTTATCAGAGGCAATG 2373
Db 1417 TGAAGCCTTCATATTTGGTCAAGAGCAAAAGAAATTTATGAGGATTTATCAGAGGGCAATG 1476
Qy 2374 TTAATGAAATATTTAGTTTATGTCAAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAA 2433
Db 1477 TTAATGAAATATTTAGTTTATGTCAAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAA 1536
Qy 2434 AAGAAGCCATPAAGATTTAGTTTATGTCAAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAA 2493
Db 1537 AAGAAGCCATPAAGATTTAGTTTATGTCAAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAA 1596
Qy 2494 AGGCTTTGAGAAATTTGTCATTTGACATATATGAGGTCAGATTTACTTGCCTTACTTTGGCC 2553
Db 1597 AGGCTTTGAGAAATTTGTCATTTGACATATATGAGGTCAGATTTACTTGCCTTACTTTGGCC 1656
Qy 2554 ACAGTGAACAGGAAGAGTAGTATGATGAATATTTCTTGTGAGCTCTGCCACCTTCTG 2613
Db 1657 ACAGTGAACAGGAAGAGTAGTATGATGAATATTTCTTGTGAGCTCTGCCACCTTCTG 1716
Qy 2614 ATGGCTTTGCATCTATATATATGACACAGAGCTCTCAGAAATAGATGAATTTTGAAGCAA 2673
Db 1717 ATGGCTTTGCATCTATATATGACACAGAGCTCTCAGAAATAGATGAATTTTGAAGCAA 1776
Qy 2674 GAAAAATGATTTGGCATTTGTCACAGATTAGATATACACTTTTGATTTTTCACAGTAGAAG 2733
Db 1777 GAAAAATGATTTGGCATTTGTCACAGATTAGATATACACTTTTGATTTTTCACAGTAGAAG 1836
Qy 2734 AAAATTTATCAATTTGGCTTCAATCAAGGGATACCAGCCAAATATTAATACAGAAAG 2793
Db 1837 AAAATTTATCAATTTGGCTTCAATCAAGGGATACCAGCCAAATATTAATACAGAAAG 1896
Qy 2794 TGCAGAGGTTTACTAGATTTAGACATCGAGCTATCAAAAGATAACCAAGCTTAAATAAT 2853
Db 1897 TGCAGAGGTTTACTAGATTTAGACATCGAGCTATCAAAAGATAACCAAGCTTAAATAAT 1956
Qy 2854 TAAGTGTGTGTCFAAAAAAGAAAGCTGTATTAGAAATGTCTTTTGGGAAACCCAAAGA 2913
Db 1957 TAAGTGTGTGTCFAAAAAAGAAAGCTGTATTAGAAATGTCTTTTGGGAAACCCAAAGA 2016
Qy 2914 TACTGCTGTAGTAGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGA 2973
Db 2017 TACTGCTGTAGTAGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGA 2076
Qy 2974 ATCTTTTAAATACAGAAAGCCAAATCGGTTGACAGTGTTCAGTACTCATTTTCATGGATG 3033
Db 2077 ATCTTTTAAATACAGAAAGCCAAATCGGTTGACAGTGTTCAGTACTCATTTTCATGGATG 2136
Qy 3034 AAGCTGACATTTGTCAGATAGGAAAGCTGTGATATCAAGGAATGCTGAAATGTGTTG 3093
Db 2137 AAGCTGACATTTGTCAGATAGGAAAGCTGTGATATCAAGGAATGCTGAAATGTGTTG 2196
Qy 3094 GTTCTTCAATGTCTCTCAAAAGTAAATGGGGGATCGGCTACCGCTCAGCATGTACATAG 3153
Db 2197 GTTCTTCAATGTCTCTCAAAAGTAAATGGGGGATCGGCTACCGCTCAGCATGTACATAG 2256
Qy 3154 ACAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTTAAACACATATACCTGGAGCTA 3213
Db 2257 ACAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTTAAACACATATACCTGGAGCTA 2316
Qy 3214 CTTTATTACAGAAATGACCAACAACTGTGTATAGCTTGCCTTCAAGGACATGGACA 3273
Db 2317 CTTTATTACAGAAATGACCAACAACTGTGTATAGCTTGCCTTCAAGGACATGGACA 2376
Qy 3274 AATTTTCAGGTTTGTCTTCTGCCCTAGACAGTCAATTCAAATTTGGGTCTCATTTCTTATG 3333
Db 2377 AATTTTCAGGTTTGTCTTCTGCCCTAGACAGTCAATTCAAATTTGGGTCTCATTTCTTATG 2436
Qy 3334 GTGTTTCCATGACGATTTGGAGACGTTATTTTAAAGCTAGAGTTCAAGCAGAAATG 3393
Db 2437 GTGTTTCCATGACGATTTGGAGACGTTATTTTAAAGCTAGAGTTTAAAGCAGAAATG 2496

Qy 3394 ACCAAGCAGATTATAGTGTATTTTACTCAGCAGCCACTGGAGGAAGAAATGGAATTCAAAAT 3453
Db 2497 ACCAAGCAGATTATAGTGTATTTTACTCAGCAGCCACTGGAGGAAGAAATGGAATTCAAAAT 2556
Qy 3454 CTTTGTAGAAATGGAAACAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTCTCTAGTGA 3513
Db 2557 CTTTGTAGAAATGGAAACAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTCTCTAGTGA 2616
Qy 3514 GCACCATCAGCCTTTGGAAACAAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCT 3573
Db 2617 GCACCATCAGCCTTTGGAAACAAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCT 2676
Qy 3574 TGAACCGTGAAGTAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAG 3633
Db 2677 TGAACCGTGAAGTAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAG 2736
Qy 3634 TTTCAGATTTTATGTTTGTGTTTCTCATCTCTTTTAAAAATGCTGTGTTCCCATCAAC 3693
Db 2737 TTTCAGATTTTATGTTTGTGTTTCTCATCTCTTTTAAAAATGCTGTGTTCCCATCAAC 2796
Qy 3694 TTGTTCCAGACTTATATTTTCTAAAACTGGAGACAAACCAATATAACAAACAGTCT 3753
Db 2797 TTGTTCCAGACTTATATTTTCTAAAACTGGAGACAAACCAATATAACAAACAGTCT 2856
Qy 3754 TGCCTTTTCAAAATTTCTGCTGACTCAGATATCAGTATCTTATAGCTTTTTCACAAGCC 3813
Db 2857 TGCCTTTTCAAAATTTCTGCTGACTCAGATATCAGTATCTTATAGCTTTTTCACAAGCC 2916
Qy 3814 AGAACATATGCTGACGATGATTAATGACGACTATGTATCCGTGCTCCCATATGTG 3873
Db 2917 AGAACATATGCTGACGATGATTAATGACGACTATGTATCCGTGCTCCCATATGTG 2976
Qy 3874 CGGCTTTAAATGATGATTCAGAAAAGGACTATGTTTTGCGAGCTGTTTTCAACAGTA 3933
Db 2977 CGGCTTTAAATGATGATTCAGAAAAGGACTATGTTTTGCGAGCTGTTTTCAACAGTA 3036
Qy 3934 CTATGTTTTATTTCTTTTACCTATATTAGTGAATATCATTTAGTAACTACTATCTTTATCAT 3993
Db 3037 CTATGTTTTATTTCTTTTACCTATATTAGTGAATATCATTTAGTAACTACTATCTTTATCAT 3096
Qy 3994 TAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATCTTTTCAAGAAATTTACTGATA 4053
Db 3097 TAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATCTTTTCAAGAAATTTACTGATA 3156
Qy 4054 TAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGAATCATTTGTACTGCAA 4113
Db 3157 TAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGAATCATTTGTACTGCAA 3216
Qy 4114 TGCACCTTTACTTTTGCATGGAATTCAGAGAATCATAGAATCAAAAGCTTATATCTCAAC 4173
Db 3217 TGCACCTTTACTTTTGCATGGAATTCAGAGAATCATAGAATCAAAAGCTTATATCTCAAC 3276
Qy 4174 TTAACCTTTCAGGCTCTTTTGCATCTGCATATTGGATTGGACAAGCTGTTGTATATCC 4233
Db 3277 TTAACCTTTCAGGCTCTTTTGCATCTGCATATTGGATTGGACAAGCTGTTGTATATCC 3336
Qy 4234 CCTTATTTTATCATCTTATTTTGAATGCTAGGAAGCTTACTGGCATTTCAATTTATGGAAT 4293
Db 3337 CCTTATTTTATCATCTTATTTTGAATGCTAGGAAGCTTATTTGGCATTTCAATTTATGGAAT 3396
Qy 4294 TATATTTTATACGTAAAGTCTCTTCTGCTGCTGTTTTTGGCTTATTTGCTTATGTTCCAT 4353
Db 3397 TATATTTTATACGTAAAGTCTCTTCTGCTGCTGTTTTTGGCTTATTTGCTTATGTTCCAT 3456
Qy 4354 CAGTTATCTGTTTCACTTATATTTTCTTCACTTTTAAAGAAATTTTAAATACCAAG 4413
Db 3457 CAGTTATCTGTTTCACTTATATTTTCTTCACTTTTAAAGAAATTTTAAATACCAAG 3516
Qy 4414 AATTTTGGTCATTTATCTATTTCTGTGGCAGCTGTTGTTGTTGTAATGCAATCACTGAAATAA 4473
Db 3517 AATTTTGGTCATTTATCTATTTCTGTGGCAGCTGTTGTTGTTGTAATGCAATCACTGAAATAA 3576

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 25, 2888, 2889
OTHER INFORMATION: n = A, T, C or G
US-10-090-458-1

Query Match 80.5%; Score 5255.8; DB 13; Length 5463;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 5340; Conservative 8; Mismatches 50; Gaps 3;

QY	994	AGGTTTATTCAGAAACATGCCACATGCAATAGGAGGAGTAGGAGTTGGAGACAGACCA	1053
DB	97	AGGTTTATTCAGAAACATGCCACATGCAATAGGAGGAGTAGGAGTTGGAGACAGACCA	156
QY	1054	GAACACCTTCTACTGAAGAAATCTTAAATTAATGAGAAACCAAAAGAGTAGTGTTCAGG	1113
DB	157	GAACACCTTCTACTGAAGAAATCTTAAATTAATGAGAAACCAAAAGAGTAGTGTTCAGG	216
QY	1114	AAATCTTTTCCACTATTTTTTTTATTTTGGTTAATTAATTAATGAGCATGATGCCAA	1173
DB	217	AAATCTTTTCCACTATTTTTTTTATTTTGGTTAATTAATTAATGAGCATGATGCCAA	276
QY	1174	ATAGAAATATGAAGAGTGCTAAATATAGAACTCAATCCTATGGACAAAGTTTACTCTTT	1233
DB	277	ATAAGAAATATGAAGAGTGCTAAATATAGAACTCAATCCTATGGACAAAGTTTACTCTTT	336
QY	1234	CTAATCTAATTCCTTGGATATCTCCAGTACTAATATTAACAGCAGCATCATGCAAGAG	1293
DB	337	CTAATCTAATTCCTTGGATATCTCCAGTACTAATATTAACAGCAGCATCATGCAAGAG	396
QY	1294	TGCTCTACTGATCATCTCCTTAAGCCGAGCAACCTTTGAGTGTGGTTTCAAAAGAGAAA	1353
DB	397	TGCTCTACTGATCATCTCCTTAAGCCGAGCAACCTTTGAGTGTGGTTTCAAAAGAGAAA	456
QY	1354	TGTTAAACATCCAGTCTCTCTAAGCCGAGCAACCTTTGAGTGTGGTTTCAAAAGACTCCA	1413
DB	457	TGTTAAACATCCAGTCTCTCTAAGCCGAGCAACCTTTGAGTGTGGTTTCAAAAGACTCCA	516
QY	1414	TGCTCTATGAACTTGGTTTTTCTGATGATGATCCAGTATCTTCTATTATATGATT	1473
DB	517	TGCTCTATGAACTTGGTTTTTCTGATGATGATCCAGTATCTTCTATTATATGATT	576
QY	1474	CAAGAGCTGGTGTTCAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTTCACAG	1533
DB	577	CAAGAGCTGGTGTTCAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTTCACAG	636
QY	1534	TTTTCAAGCATCCATAGATGCTGCCATATACAGTTGAAGACCAATGTTTCTCTTGGGA	1593
DB	637	TTTTCAAGCATCCATAGATGCTGCCATATACAGTTGAAGACCAATGTTTCTCTTGGGA	696
QY	1594	AGGAGCTGGAGTCACTAAAGCTGTTATATGGGAGAACTGCTGTTGTAGAAATAGATA	1653
DB	697	AGGAGCTGGAGTCACTAAAGCTGTTATATGGGAGAACTGCTGTTGTAGAAATAGATA	756
QY	1654	CTTTTCCCGAGGAGTAATTTTAAATACCTAGTTATAGCAATTTACCTTTTGATACT	1713
DB	757	CTTTTCCCGAGGAGTAATTTTAAATACCTAGTTATAGCAATTTACCTTTTGATACT	816
QY	1714	TTTTGGCAATTCATATCGTAGCAGAAAAGAAAAGAAAATTAAGATAA	1773
DB	817	TTTTGGCAATTCATATCGTAGCAGAAAAGAAAAGAAAATTAAGATAA	876
QY	1774	TGGGACTTCATGATACTGCTTTTGGCTTTCTGGGTTCTTCTATATACAGTTTAAATTT	1833
DB	877	TGGGACTTCATGATACTGCTTTTGGCTTTCTGGGTTCTTCTATATACAGTTTAAATTT	936
QY	1834	TTCTTATGTCCTTCTTATGGCAGTCATTCGACAGCTTCTTGTATTTCTCTCAAGTA	1893
DB	937	TTCTTATGTCCTTCTTATGGCAGTCATTCGACAGCTTCTTGTATTTCTCTCAAGTA	996
QY	1894	GCAGCATGTGATATTTCTGCTTTTCTTTTATGGATATCATCTGATTTTGTGCTT	1953

DB	997	GCAGCATGTGATATTTCTGCTTTTCTTTTATGGATATCATCTGATATTTTGTGCTT	1056
QY	1954	TAATGCTCACACCTCTTTTAAAAAATCAAAACATGCGGAATAGTTCGAATTTTGTTA	2013
DB	1057	TAATGCTCACACCTCTTTTAAAAAATCAAAACATGCGGAATAGTTCGAATTTTGTTA	1116
QY	2014	CTGTGGCTTTTGGATTTATTTGGCTTATGATAAATCTCATAGAAAGTTTCCCAATCGT	2073
DB	1117	CTGTGGCTTTTGGATTTATTTGGCTTATGATAAATCTCATAGAAAGTTTCCCAATCGT	1176
QY	2074	TAGTGTGGCTTTTTCAGTCTTCTGCTACTGTACTTTTGTGATTTGATTCACAGGTCA	2133
DB	1177	TAGTGTGGCTTTTTCAGTCTTCTGCTACTGTACTTTTGTGATTTGATTCACAGGTCA	1236
QY	2134	TGCATTTAGAAATTTAATGAAGTCTTCAATTTTCAAAATTTGACTCGAGGCCATATC	2193
DB	1237	TGCATTTAGAAATTTAATGAAGTCTTCAATTTTCAAAATTTGACTCGAGGCCATATC	1296
QY	2194	CTCTAATTTATCAATTTATCATGCTCACATTAATAGTATATTTCTATGCTCTTGGCTG	2253
DB	1297	CTCTAATTTATCAATTTATCATGCTCACATTAATAGTATATTTCTATGCTCTTGGCTG	1356
QY	2254	TCTATCTTGATCAAGTCAATCCAGGGAAATTTGGCTTACGGAGATCATCTTTATTTTC	2313
DB	1357	TCTATCTTGATCAAGTCAATCCAGGGAAATTTGGCTTACGGAGATCATCTTTATTTTC	1416
QY	2314	TGAAGCTTTCAATTTGGTCAAAAGAGTAAAAAGAAATTTATGAGAGTTATCAGAGGCAATG	2373
DB	1417	TGAAGCTTTCAATTTGGTCAAAAGAGTAAAAAGAAATTTATGAGAGTTATCAGAGGCAATG	1476
QY	2374	TTAATGGAAATTTAGTTTGTAGTAAATTTATGAGCCAGTTTCTTCAGAAATTTAGGAA	2433
DB	1477	TTAATGGAAATTTAGTTTGTAGTAAATTTATGAGCCAGTTTCTTCAGAAATTTAGGAA	1536
QY	2434	AGAAGCCATAGAAATTTAGTGTATTTAGAAACATACAGAAAGAGGGTGAATTTGCGG	2493
DB	1537	AGAAGCCATAGAAATTTAGTGTATTTAGAAACATACAGAAAGAGGGTGAATTTGCGG	1596
QY	2494	AGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAAGTTACTGCTTACTTGGCC	2553
DB	1597	AGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAAGTTACTGCTTACTTGGCC	1656
QY	2554	ACGTGGAACAGAAAGAGTACATTTGATGAATATTTCTTTGTGAGCTCTGCCACCTTCG	2613
DB	1657	ACGTGGAACAGAAAGAGTACATTTGATGAATATTTCTTTGTGAGCTCTGCCACCTTCG	1716
QY	2614	ATGGGTTTGCATCTATATATGACACAGAGTCTCAGAAATAGATGAAATTTTGAAGCAA	2673
DB	1717	ATGGGTTTGCATCTATATATGACACAGAGTCTCAGAAATAGATGAAATTTTGAAGCAA	1776
QY	2674	GAAAAATGATTTGGCAATTTGTCCACAGTTAGATATACATTTTGTGATGTTTGTGACAGTAGAAG	2733
DB	1777	GAAAAATGATTTGGCAATTTGTCCACAGTTAGATATACATTTTGTGATGTTTGTGACAGTAGAAG	1836
QY	2734	AAAAATTTATCAATTTTGGCTTCAATCAAAGGGATACCGCAACAAATATAATCAAGAAAG	2793
DB	1837	AAAAATTTATCAATTTTGGCTTCAATCAAAGGGATACCGCAACAAATATAATCAAGAAAG	1896
QY	2794	TGCAGAAAGTTTCTACTAGATTTTAGACATGCAGACTATCAAGAGTAAACCAAGCTTAAAAAT	2853
DB	1897	TGCAGAAAGTTTCTACTAGATTTTAGACATGCAGACTATCAAGAGTAAACCAAGCTTAAAAAT	1956
QY	2854	TAAGTGGTGTCAAAAAGAAAGAGCTGCTCATTTAGGATTTGCTGTTCTTTGGAAACCCAAAGA	2913
DB	1957	TAAGTGGTGTCAAAAAGAAAGAGCTGCTCATTTAGGATTTGCTGTTCTTTGGAAACCCAAAGA	2016
QY	2914	TACTGCTGTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTTGTATGGA	2973
DB	2017	TACTGCTGTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTTGTATGGA	2076
QY	2974	ATCTTTTAAATACAGAAAGCCAAATCGGTTGACAGTGTTCAGTACTCATTTTCATGGATG	3033
DB	2077	ATCTTTTAAATACAGAAAGCCAAATCGGTTGACAGTGTTCAGTACTCATTTTCATGGATG	2136

QY 3034 AAGCTGACATCTTGCAGATAGAAAGCTGATATCAAGGAATGCTGAAATGTTG 3093
Db 2137 AAGCTGACATCTTGCAGATAGAAAGCTGATATCAAGGAATGCTGAAATGTTG 2196
QY 3094 GTTCTTCAATGTTCTCTCAAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAG 3153
Db 2197 GTTCTTCAATGTTCTCTCAAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAG 2256
QY 3154 ACAATATTTGTCACAGATCTCTTTCTTCACTGGTTAAACAACATATACCTGAGCTA 3213
Db 2257 ACAATATTTGTCACAGATCTCTTTCTTCACTGGTTAAACAACATATACCTGAGCTA 2316
QY 3214 CTTTATTACAAAGATGACCAACACTTGTGTATAGTTGCTTCAAGGACATGGACA 3273
Db 2317 CTTTATTACAAAGATGACCAACACTTGTGTATAGTTGCTTCAAGGACATGGACA 2376
QY 3274 AATTTTCAGGTTGTTTCTGCGCTAGACAGTCAATCAAAATTTGGGTGTCAATTCCTATG 3333
Db 2377 AATTTTCAGGTTGTTTCTGCGCTAGACAGTCAATCAAAATTTGGGTGTCAATTCCTATG 2436
QY 3334 GTGTTTCCATGACGACTTTGGAAGAGCTATTTTAAAGCTAGAAGTTGAAGCAGAAATG 3393
Db 2437 GTGTTTCCATGACGACTTTGGAAGAGCTATTTTAAAGCTAGAAGTTGAAGCAGAAATG 2496
QY 3394 ACCAAGCAGATATAGTGTATTACTCAGCAGCCACTGGAGGAAGAAATGGATCAAAAT 3453
Db 2497 ACCAAGCAGATATAGTGTATTACTCAGCAGCCACTGGAGGAAGAAATGGATCAAAAT 2556
QY 3454 CTTTTCATGAATGGAACAGCTTACTTATCTTCTGAAACCAAGGCTTCTAGTGA 3513
Db 2557 CTTTTCATGAATGGAACAGCTTACTTATCTTCTGAAACCAAGGCTTCTAGTGA 2616
QY 3514 GCACCATGAGCCTTTGGAACCAACAGATATACAAATAGCAAAAGTTTCATTTCTTACCT 3573
Db 2617 GCACCATGAGCCTTTGGAACCAACAGATATACAAATAGCAAAAGTTTCATTTCTTACCT 2676
QY 3574 TGAACGTGAAGTAAATCAGTGAGATCAGTGTGCTGCTGCTTTTAAATTTTTCACAG 3633
Db 2677 TGAACGTGAAGTAAATCAGTGAGATCAGTGTGCTGCTGCTTTTAAATTTTTCACAG 2736
QY 3634 TTCAGATTTTATGTTTGGTTTCATCACTCTTTTAAATAATGCTGTGTTCCCATCAAC 3693
Db 2737 TTCAGATTTTATGTTTGGTTTCATCACTCTTTTAAATAATGCTGTGTTCCCATCAAC 2796
QY 3694 TTGTTCCAGACTTATATTTCTAAACCTGGAGACAAACACATATAACAAACAGTC 3753
Db 2797 TTGTTCCAGACTTATATTTCTAAACCTGGAGACAAACACATATAACAAACAGTC 2856
QY 3754 TCGTCTTCAAAATCTGCT-----GACTCAGATATCAGTGATCTTA 3795
Db 2857 TCGTCTTCAAAATCTGCTGGTGAGAGTGTGNGTGAAGACTCAGATATCAGTGATCTTA 2916
QY 3796 TTAGCTTTTTCACAGCCAGACATAATGGTGACGATGATTAATCAGAGTACTATGAT 3855
Db 2917 TTAGCTTTTTCACAGCCAGACATAATGGTGACGATGATTAATCAGAGTACTATGAT 2976
QY 3856 CCGTGGCTCCCATAGTGGGCTTTAAATGTCATGCTCATTGACAAAGGACTATGTTTTG 3915
Db 2977 CCGTGGCTCCCATAGTGGGCTTTAAATGTCATGCTCATTGACAAAGGACTATGTTTTG 3036
QY 3916 CAGCTTTTTCACAGTACTATGTTTATTTCTTTACCTATATTTAGTGAATATCATAGTA 3975
Db 3037 CAGCTTTTTCACAGTACTATGTTTATTTCTTTACCTATATTTAGTGAATATCATAGTA 3096
QY 3976 ACTACTATCTTATCATTTTAAATGTCATGAACCATCCAGATCTGGAGTACCCCATTTCT 4035
Db 3097 ACTACTATCTTATCATTTTAAATGTCATGAACCATCCAGATCTGGAGTACCCCATTTCT 3156
QY 4036 TTCAAGAAATTTACTGATATAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTG 4095
Db 3157 TTCAAGAAATTTACTGATATAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTG 3216

QY 4096 G-AATCATTTGTTACTGCAATGCCACCTTACTTTGCCATGAAAAATGAGAGAAATCATAG 4154
Db 3217 GAAATCATTTGTTAACTGCAATGCCACCTTACTCTGCCATGAAAAATGAGAGAAATCAT- 3274
QY 4155 ATCAAGCTTTATACTCAACTTAAACTTTCAAGTCTTTTGGCATCTGCAATTTGGATTGA 4214
Db 3275 -----AGGTCCTTTTGGCATCTGCAATTTGGATTGA 3305
QY 4215 CAAGCTGTTGTTGATATCCCTTTATTTTATCATTTTATTTGATGCTAGGAAGCTTA 4274
Db 3306 CAAGCTGTTGTTGATATCCCTTTATTTTATCATTTTATTTGATGCTAGGAAGCTTA 3365
QY 4275 CTGCAATTTCAATPATGGATATATTTTATACGTAAAGTCTCTGCTGTGGTTTTTGC 4334
Db 3366 TTGCAATTTCAATPATGGATATATTTTATACGTAAAGTCTCTGCTGTGGTTTTTGC 3425
QY 4335 CTTTATTTGTTTATCTTCCATCAGTATTTCTGTTCACTTATATTTGCTTTTCACTTTAAG 4394
Db 3426 CTTTATTTGTTTATGTTTCCATCAGTATTTCTGTTCACTTATATTTGCTTTTCACTTTAAG 3485
QY 4395 AAAATTTTAAATACCAAGAAATTTTGGTCATTTATCTATTTCTGTGGCAGGTTGCTTGT 4454
Db 3486 AAAATTTTAAATACCAAGAAATTTTGGTCATTTATCTATTTCTGTGGCAGGTTGCTTGT 3545
QY 4455 ATTGCAATCACTGAAATTAATTTTCTTTATGGGATACAAATTCACACTATTTCTTCAATTAT 4514
Db 3546 ATTGCAATCACTGAAATTAATTTTCTTTATGGGATACAAATTCACACTATTTCTTCAATTAT 3605
QY 4515 GCCTTTTGTATCATCATTTCCAATCTATCCACTTTAGTGTGCTGATTTCTTTCAATAAG 4574
Db 3606 GCCTTTTGTATCATCATTTCCAATCTATCCACTTTAGTGTGCTGATTTCTTTCAATAAG 3665
QY 4575 ATTTCTTTGGAAGATGTACGAAAAATGTGGACACCTATAATCCATGGATAGGCTTTTCA 4634
Db 3666 ATTTCTTTGGAAGATGTACGAAAAATGTGGACACCTATAATCCATGGATAGGCTTTTCA 3725
QY 4635 GTAGCTGTTATATCGCTTACCTGCAAGTGTGACTGTGATTTTCTCTTACAATACTAT 4694
Db 3726 GTAGCTGTTATATCGCTTACCTGCAAGTGTGACTGTGATTTTCTCTTACAATACTAT 3785
QY 4695 GAGAAAAATATCGAGGAGATCAATAAGAAAAAGATCCCTTTTTCAGAAAACTTTTCAAGC 4754
Db 3786 GAGAAAAATATCGAGGAGATCAATAAGAAAAAGATCCCTTTTTCAGAAAACTTTTCAAGC 3845
QY 4755 AAGCTTAAATAAGGAGCTTCCAGAACCAACAGCAATGAGATGAAGATGATGTC 4814
Db 3846 AAGCTTAAATAAGGAGCTTCCAGAACCAACAGCAATGAGATGAAGATGATGTC 3905
QY 4815 AAAGCTGAAAGACTAAAGGCTCAAAGAGCTGATGGGTGCGAGTGTGTCAGGAGAAACCA 4874
Db 3906 AAAGCTGAAAGACTAAAGGCTCAAAGAGCTGATGGGTGCGAGTGTGTCAGGAGAAACCA 3965
QY 4875 TCCATTTATGTCAGCAATTTGCAATAAGATATGATGACAAAGAAATTTCTTCTTTTCA 4934
Db 3966 TCCATTTATGTCAGCAATTTGCAATAAGAAATATGATGACAAAGAAATTTCTTCTTTTCA 4025
QY 4935 AGAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTGTGTGAAAAAGAGAGATC 4994
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RESULT 6
US-09-971-121-1
; Sequence 1, Application US/09971121
; Patent No. US20020111477A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomichy, Boris
; TITLE OF INVENTION: No. US20020111477A1 Human Transporter Proteins and Polynucleot
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4929
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-971-121-1

Query Match 75.4%; Score 4918.4; DB 9; Length 4929;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4919; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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Qy 2691 TGTCCACAGTTAGATATACATTTGATGTTTTCACAGTAGAAGAAATTTATCAATTTG 2750
Db 1681 TGTCCACAGTTAGATATACATTTGATGTTTTCACAGTAGAAGAAATTTATCAATTTG 1740
Qy 2751 GCTTTCAATCAAGGGATACAGCAACAATATATAACAAGTGCAGAAAGTTTACTA 2810
Db 1741 GCTTTCAATCAAGGGATACAGCAACAATATATAACAAGTGCAGAAAGTTTACTA 1800
Qy 2811 GATTTAGACATGACAGTATCAAGATACCAAGCTTAAATAATTAAGTGGTCAAAA 2870
Db 1801 GATTTAGACATGACAGTATCAAGATACCAAGCTTAAATAATTAAGTGGTCAAAA 1860
Qy 2871 AGAAAGCTGTCATTTAGGAATGCTGTTCTTTGGAAACCAAGATATCTGCTGATGAA 2930
Db 1861 AGAAAGCTGTCATTTAGGAATGCTGTTCTTTGGAAACCAAGATATCTGCTGATGAA 1920
Qy 2931 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATGTTATGGAATCTTTTAAATAACAG 1980
Db 2991 AAGCCAAATCGGGTACAGTCTTCTGACATATTTGATGGAATCTTTTAAATAACAG 2040
Qy 3051 GATAGGAAAGCTGATATCAAGAAATGCTGAAATGCTGTTGCTTCAATGTTCTC 3110
Db 2041 GATAGGAAAGCTGATATCAAGAAATGCTGAAATGCTGTTGCTTCAATGTTCTC 2100
Qy 3111 AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTTGGCCACA 3170
Db 2101 AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTTGGCCACA 2160
Qy 3171 GAATCTCTTTCTTCACTGGTTAAACAAATATACCTGGAGCTACTTTTATTAACAAGAA 3230
Db 2161 GAATCTCTTTCTTCACTGGTTAAACAAATATACCTGGAGCTACTTTTATTAACAAGAA 2220
Qy 3231 GACCAACAACTGTGTATAGCTTGCCTTCAAGACATGACAAATTTTCAAGTTGTTT 3290
Db 2221 GACCAACAACTGTGTATAGCTTGCCTTCAAGACATGACAAATTTTCAAGTTGTTT 2280
Qy 3291 TCTGCCCTAGACAGTCAATCAAAATTTGGGTGCTCAATTTCTTATGGTGTTCATGACGACT 3350
Db 2281 TCTGCCCTAGACAGTCAATCAAAATTTGGGTGCTCAATTTCTTATGGGTGTTCATGACGACT 2340
Qy 3351 TTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTTGACCAAGCAGATTATAGT 3410
Db 2341 TTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTTGACCAAGCAGATTATAGT 2400
Qy 3411 GTATTTACTCAGACCCACTGGAGGAAGAAATGGAATCAAAATCTTTTATGAATGAA 3470
Db 2401 GTATTTACTCAGACCCACTGGAGGAAGAAATGGAATCAAAATCTTTTATGAATGAA 2460
Qy 3471 CAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTCTCTAGTGAGCAACCATGAGCCTTGG 3530
Db 2461 CAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTCTCTAGTGAGCAACCATGAGCCTTGG 2520
Qy 3531 AAACACAGATGTATACAAATAGCAAGTTTCAATTTCTTTTACCTTGAACCGTGAAGTAAA 3590
Db 2521 AAACACAGATGTATACAAATAGCAAGTTTCAATTTCTTTTACCTTGAACCGTGAAGTAAA 2580

3591 TCACTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTT 3650
Db 2581 TCACTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTT 2640
Qy 3651 TTGCTTCATCACTCTTTTAAATAATGCTGCTCCCATCAAACTTGTTCAGACTTATAT 3710
Db 2641 TTGCTTCATCACTCTTTTAAATAATGCTGCTCCCATCAAACTTGTTCAGACTTATAT 2700
Qy 3711 TTTCTAAAACCTGGAGACAAACCAATATAAAAACAAAGTCTGCTTCTTCAAAATCT 3770
Db 2701 TTTCTAAAACCTGGAGACAAACCAATATAAAAACAAAGTCTGCTTCTTCAAAATCT 2760
Qy 3771 GCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAGCCAGAACATAAATGGTGACG 3830
Db 2761 GCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAGCCAGAACATAAATGGTGACG 2820
Qy 3831 ATGATTAATGACAGTACTATGATCGTGGCTCCCATAGTGGGCTTTAAAATGTTGATG 3890
Db 2821 ATGATTAATGACAGTACTATGATCGTGGCTCCCATAGTGGGCTTTAAAATGTTGATG 2880
Qy 3891 CATTCAGAAAAGGACTATGTTTTTGGAGCTGTTTTCAACAGTACTATGGTTATCTTTA 3950
Db 2881 CATTCAGAAAAGGACTATGTTTTTGGAGCTGTTTTCAACAGTACTATGGTTATCTTTA 2940
Qy 3951 CCTATATTAGTGAATATCATTTAGTAACCTATCTTTATCATTTTAAATGTGACTGAAACC 4010
Db 2941 CCTATATTAGTGAATATCATTTAGTAACCTATCTTTATCATTTTAAATGTGACTGAAACC 3000
Qy 4011 ATCCAGATCTGGAGTACCCCATTTCTTCAAGAAATACTGATATAGTTTTTAAATTTGAG 4070
Db 3001 ATCCAGATCTGGAGTACCCCATTTCTTCAAGAAATACTGATATAGTTTTTAAATTTGAG 3060
Qy 4071 CTGTATTTTCAAGAGCTTTGCTGGATCATTTGTTACTGCAATGCCACTTACTTTGCC 4130
Db 3061 CTGTATTTTCAAGAGCTTTGCTGGATCATTTGTTACTGCAATGCCACTTACTTTGCC 3120
Qy 4131 ATGGAAAATGCAAGAAATCAAAAGATCAAAAGCTTATCTCAACTTAAACTTTTCAAGGCTT 4190
Db 3121 ATGGAAAATGCAAGAAATCAAAAGATCAAAAGCTTATCTCAACTTAAACTTTTCAAGGCTT 3180
Qy 4191 TTGCCATCTGCATATTTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTTATCAAT 4250
Db 3181 TTGCCATCTGCATATTTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTTATCAAT 3240
Qy 4251 CTATTTTATGCTAGGAGCTTCTGTCATTTCAATTTATGGAATATATTTTATACTGTA 4310
Db 3241 CTATTTTATGCTAGGAGCTTCTGTCATTTCAATTTATGGAATATATTTTATACTGTA 3300
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Db 3301 AAGTTTCTTGTGCTGTTTTTTTGGCTTATGTTTATGTTTCAATCAGTTATCTGTTCACT 3360
Qy 4371 TATATTTGCTTCTTCACTTTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCAATTTATC 4430
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Qy 4431 TATTTCTGTGGCAGGTTGCTTGTATTTGCAATCACTGAAATTAACTTTCTTTATGGGATAC 4490
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Qy 4551 GGTGGCTGATTTCTTTTCAATAAGATTTCTTGGAGAATGTACGAAAAAATGTGGACACC 4610
Db 3541 GGTGGCTGATTTCTTTTCAATAAGATTTCTTGGAGAATGTACGAAAAAATGTGGACACC 3600
Qy 4611 TATAATCCATGGGATAGGCTTTTCAAGTGTGTTATATCGCTTACCTGAGTGTGTACTG 4670
Db 3601 TATAATCCATGGGATAGGCTTTTCAAGTGTGTTATATCGCTTACCTGAGTGTGTACTG 3660
Qy 4671 TGGATTTTCTCTTCAATACATATGAGAAAAAATATGGAGGACAGATCAATAAGAAAAAT 4730

Db 3661 TGAATTTTCTCTTACATACATATGAGAAAATATGGAGGAGATCAATAGAAAAGAT 3720
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Db 3721 CCCTTTTTCAGAAACCTTTCAACGAAGCTCAAAAATAGGAAGCTTCCAGAACCCAGAC 3780
QY 4791 AATGAGATGAAGATGAAGATCTCAAGCTGAAGCTTAAGGTCARAGAGCTGATGGT 4850
Db 3781 AATGAGATGAAGATGAAGATCTCAAGCTGAAGCTTAAGGTCARAGAGCTGATGGT 3840
QY 4851 TGCAGGTGTGTGAGAGAAACCATTCATTATGGTTCAGCAATTTGCATAAAGAAATATGAT 4910
Db 3841 TGCAGGTGTGTGAGAGAAACCATTCATTATGGTTCAGCAATTTGCATAAAGAAATATGAT 3900
QY 4911 GACAGAAAGATTTTCTCTTTTCAGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCT 4970
Db 3901 GACAGAAAGATTTTCTCTTTTCAGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCT 3960
QY 4971 TTCTGTGTCAAAAAGCAGAGATCTTAGGACTATTGGGTCCAAATGGTCTGGCAAAAGC 5030
Db 3961 TTCTGTGTCAAAAAGCAGAGATCTTAGGACTATTGGGTCCAAATGGTCTGGCAAAAGC 4020
QY 5031 ACAATTTATTAATTTCTGTGTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGGA 5090
Db 4021 ACAATTTATTAATTTCTGTGTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGGA 4080
QY 5091 GATTATTTCTTCAGAGCAAGTCAAGATGATGATTCACCTCAAGTGATGGTCTACTGTCTCT 5150
Db 4081 GATTATTTCTTCAGAGCAAGTCAAGATGATGATTCACCTCAAGTGATGGTCTACTGTCTCT 4140
QY 5151 CAGATAAACCCCTTTGTGGCCAGATACATTCATTCAGGAACATTTTGAATTTATGGAGCT 5210
Db 4141 CAGATAAACCCCTTTGTGGCCAGATACATTCATTCAGGAACATTTTGAATTTATGGAGCT 4200
QY 5211 GTCAGAGGAATGAGTCAAGTCAATGAAGAGTCAATGAAGTCAATGAAGTCAATGAAGTCAAT 5270
Db 4201 GTCAGAGGAATGAGTCAAGTCAATGAAGAGTCAATGAAGTCAATGAAGTCAATGAAGTCAAT 4260
QY 5271 GAATTTAAAGAACATCTTCAGAGAGCTGTAAAGAACTACCTGCAGGAATCAAGAGAAAG 5330
Db 4261 GAATTTAAAGAACATCTTCAGAGAGCTGTAAAGAACTACCTGCAGGAATCAAGAGAAAG 4320
QY 5331 TTGTGTGTCTCTAAGTATGCTAGGAATCTCAGATTAATTTGCTAGATGAACCATCT 5390
Db 4321 TTGTGTGTCTCTAAGTATGCTAGGAATCTCAGATTAATTTGCTAGATGAACCATCT 4380
QY 5391 ACAGGTATGATGCCAAAGCCAAACAGACATGTGGCGAGCAATTCGAACCTGCAATTTAAA 5450
Db 4381 ACAGGTATGATGCCAAAGCCAAACAGACATGTGGCGAGCAATTCGAACCTGCAATTTAAA 4440
QY 5451 AACAGAAACGGGCTGCTATTCGACCACTACTATATGGAGGCGAGAGGCTGTCTGT 5510
Db 4441 AACAGAAACGGGCTGCTATTCGACCACTACTATATGGAGGCGAGAGGCTGTCTGT 4500
QY 5511 GATCGAGTATCATATGATGTGTCTGGGAGTTTAAAGTATGCGAAGTCAACATCTA 5570
Db 4501 GATCGAGTATCATATGATGTGTCTGGGAGTTTAAAGTATGCGAAGTCAACATCTA 4560
QY 5571 AAGAGTAAATTTGAAAAGGCTACTTTTGGAAATTAATTAAGAGGCTGGATGAAAC 5630
Db 4561 AAGAGTAAATTTGAAAAGGCTACTTTTGGAAATTAATTAAGAGGCTGGATGAAAC 4620
QY 5631 CTAGAGTATGAGCGGCTTCAGAGAAATTCAGTATATTTTCCAAATGCGAGCGGCTCAG 5690
Db 4621 CTAGAGTATGAGCGGCTTCAGAGAAATTCAGTATATTTTCCAAATGCGAGCGGCTCAG 4680
QY 5691 GAAAGTATTTCTCTATTTTGGCTTATAAAATTCCTAAGGAGATGTTTCACTCCCTTTCA 5750
Db 4681 GAAAGTATTTCTCTATTTTGGCTTATAAAATTCCTAAGGAGATGTTTCACTCCCTTTCA 4740
QY 5751 CAATCTTTTTTAAGCTGAAGAGCTAAACATGCTTTTGGCAATTAAGAAATATAGCTTT 5810

RESULT 7

US-10-090-458-3
; Sequence 3, Application US/10090458
; Publication No. US20020123107A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun
; APPLICANT: Kilinski, Ligia
; APPLICANT: Le Bihan, Stephanie
; TITLE OF INVENTION: NOVEL ABCA5 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.403
; CURRENT APPLICATION NUMBER: US/10/090,458
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4917
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2775..2776
; OTHER INFORMATION: n = A, T, C or G
US-10-090-458-3

Query Match 73.7%; Score 4807.4; DB 13; Length 4917;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 4891; Conservative 0; Mismatches 7; Indels 50; Gaps 3;

QY 1011 ATGTCCACTGCAATTAGGAGGTAGGAGTTGGAGACACAGACACACATCTTCTACTGAG 1070
Db 1 ATGTCCACTGCAATTAGGAGGTAGGAGTTGGAGACACAGACACACATCTTCTACTGAG 60
QY 1071 AATTACTTAAATTAATGCGAACCCAAAGAGTAGTGTTCAGAAATTTCTTTTCCACTA 1130
Db 61 AATTACTTAAATTAATGCGAACCCAAAGAGTAGTGTTCAGAAATTTCTTTTCCACTA 120
QY 1131 TTTTCTTAAATTTGGTTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1190
Db 121 TTTTCTTAAATTTGGTTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 1191 GTCCCTAAATAGCACTCAATCTCTATGGACAAGTTTACTCTTTCTAATCTAATTTCTTGA 1250
Db 181 GTCCCTAAATAGCACTCAATCTCTATGGACAAGTTTACTCTTTCTAATCTAATTTCTTGA 240
QY 1251 TATACTCCAGTACTAATATTACAAGCAGCATCATGCAAGAAAGTGTCTACTCATCTA 1310
Db 241 TATACTCCAGTACTAATATTACAAGCAGCATCATGCAAGAAAGTGTCTACTCATCTA 300
QY 1311 CCTGATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1370
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QY 1371 TCTAAGCCGAGCAACTTTTGTAGTGTGGTTTCAAAGACTCCCATGCTTATGAACCTCT 1430
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QY 1431 TTTTCTTCTGATATGATCCAGTATCTTCTATTTATGATTAAGATTAAGAGCTGGCTGTCA 1490

Db 421 TTTTTCCTGATGATCCAGTATCTTCTATTATATGGAATCAAGAGCTGGCTTTCA 480
 Qy 1491 AATCATGTGAGCTCTCAGTACTGCTCCTCAGGTTTACAGTATTTTACAAGCATCCATA 1550
 Db 481 AATCATGTGAGCTCTCAGTACTGCTCCTCAGGTTTACAGTATTTTACAAGCATCCATA 540
 Qy 1551 GATGCTGCCATTATACAGTTGAAGCAATGTTTCTTTTGAAGGAGCTGGAGTCAACT 1610
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 Qy 1611 AAGCTGTTATTATGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGAGTA 1670
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 Qy 1671 ATTTTAATACCTAGTTATAGCATTTTACCTTTTGGATACCTTTTGGCAATTCATATC 1730
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 Qy 1731 GTAGCAAAAGAAAATAAAGAAATTTTAAAGATAATGGAGCTTCATGATACT 1790
 Db 721 GTAGCAAAAGAAAATAAAGAAATTTTAAAGATAATGGAGCTTCATGATACT 780
 Qy 1791 GCCTTTTGGCTTCTCGGTTCTCTATATACAAAGTTTAAATTTTCTTATGTCCTTCTT 1850
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 Qy 1911 CTGCTTTTTCCTTTTGGATTATCATCTGATTTTTTGGCTTTAAATGCTGACACCTCTT 1970
 Db 901 CTGCTTTTTCCTTTTGGATTATCATCTGATTTTTTGGCTTTAAATGCTGACACCTCTT 960
 Qy 1971 TTTAAAAAATCAAAACATGTCGGAATAGTTGAATTTTTTGTACTGTCGGCTTTGGATTT 2030
 Db 961 TTTAAAAAATCAAAACATGTCGGAATAGTTGAATTTTTTGTACTGTCGGCTTTGGATTT 1020
 Qy 2031 ATTGSCCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGCTTTTCAGT 2090
 Db 1021 ATTGSCCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGCTTTTCAGT 1080
 Qy 2091 CCTTCTGCTGCTGACCTTTTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2150
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 Qy 2151 AATGAAGTGCTTCAATTTCAAAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2210
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 Qy 2211 ATCATGCTCAGACTTAATAGTATATTTCTATGCTTGGCTGCTATCTTTGATCAAGTC 2270
 Db 1201 ATCATGCTCAGACTTAATAGTATATTTCTATGCTTGGCTGCTATCTTTGATCAAGTC 1260
 Qy 2271 ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTTATATTTTCTGAAGCCTTCATATGG 2330
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 Db 1381 TTTAGTGAATTTATGAGCCAGTTCTTCTCAGAAATTTGTAGGAAAAGAGCCATAGAATTT 1440
 Qy 2451 AGTGGTATTCAGAAGCATACAGAAAGAGGTGAATTTGAGAGGCTTTGAGAAATTTG 2510
 Db 1441 AGTGGTATTCAGAAGCATACAGAAAGAGGTGAATTTGAGAGGCTTTGAGAAATTTG 1500
 Qy 2511 TCATTTGACATATACAGGGTTCAGATTCTGCTTACTTTGGCCACAGTGGAAACAGGAAAG 2570
 Db 1501 TCATTTGACATATACAGGGTTCAGATTCTGCTTACTTTGGCCACAGTGGAAACAGGAAAG 1560

Qy 2571 AGTACATTGATGAATATATCTTTTGGACTCTGCCACCTTCTGATGGTTTGCATCTATA 2630
 Db 1561 AGTACATTGATGAATATATCTTTTGGACTCTGCCACCTTCTGATGGTTTGCATCTATA 1620
 Qy 2631 TATGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAAATGATTTGGCAAT 2690
 Db 1621 TATGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAAATGATTTGGCAAT 1680
 Qy 2691 TGTCCACAGTTAGATATACATCTTTGATGTTTGGACTGACAGTGAAGAAAATTTATCAATTTG 2750
 Db 1681 TGTCCACAGTTAGATATACATCTTTGATGTTTGGACTGACAGTGAAGAAAATTTATCAATTTG 1740
 Qy 2751 GCTTCAATCAAGGGATACCAAGCAATATAATACAAAGAGTGCAGAGAGTTTACTA 2810
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 Qy 2811 GATTTAGACATGACAGCTATCAAGATAAACAAAGTAAAAAATTAAGTGGTGGTCAAAA 2870
 Db 1801 GATTTAGACATGACAGCTATCAAGATAAACAAAGTAAAAAATTAAGTGGTGGTCAAAA 1860
 Qy 2871 AGAAGAGCTGCTANTAGGAATTCCTGTTCTGGGACCCCAAGATACCTCTCTAGATCAA 2930
 Db 1861 AGAAGAGCTGCTANTAGGAATTCCTGTTCTGGGAAACCCCAAGATACCTCTCTAGATGAA 1920
 Qy 2931 CCAACAGCTGGAATGAGACCCCTGTTCTCGACATATTTGTATGGAATCTTTTAAAAATACAGA 2990
 Db 1921 CCAACAGCTGGAATGAGACCCCTGTTCTCGACATATTTGTATGGAATCTTTTAAAAATACAGA 1980
 Qy 2991 AAGCCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATCTTGA 3050
 Db 1981 AAGCCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATCTTGA 2040
 Qy 3051 GATAGAAAGCTGTGATATCAAGAAATGTCGAAATGTTGGTTCCTTCAATGTTCTCT 3110
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 Qy 3171 GAATCTCTTCTCTCACTGCTTAAACAAATATACCTGAGCTACTTTTATTAACAAGAAAT 3230
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 Db 2221 GACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGAACAAATTTTCAAGTTTGT 2280
 Qy 3291 TCTGCCCCTAGACAGTCAATCAAAATTTGGGTGCTCATTTCTTATGTTGTTTCCATGAGACT 3350
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 Qy 3411 GTATTTTCTCAGAGCCACTGGAGGAAGAAATGGATTTCAAAATCTTTTGAATGAATGAA 3470
 Db 2401 GTATTTTCTCAGAGCCACTGGAGGAAGAAATGGATTTCAAAATCTTTTGAATGAATGAA 2460
 Qy 3471 CAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTCTAGTGAAGCAAGCTTGG 3530
 Db 2461 CAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTCTAGTGAAGCAAGCTTGG 2520
 Qy 3531 AAAACAACAGATGATACAAATAGCAAAAGTTTCAATTTCTTCTTAAACCTGAAAGTAAA 3590
 Db 2521 AAAACAACAGATGATACAAATAGCAAAAGTTTCAATTTCTTCTTAAACCTGAAAGTAAA 2580
 Qy 3591 TCAGTGAATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAAGTTTATGTTT 3650
 Db 2581 TCAGTGAATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAAGTTTATGTTT 2640

QY 3651 TTGGTTTCATCACTCTTTTAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATAT 3710
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QY 3711 TTTCTAAACCTGGAGACAAACACATAAATACAAACAAAGTCTGCTTCTTCAAAATCT 3770
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QY 3813 CAGAAATATGCTGACGATGATTAATGACAGTGACTATGATTCGGTGGCTCCCATAGT 3872
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QY 3873 GCGGCTTTAAATGCTGATGATTCAGAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGT 3932
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QY 3933 ACTATGGTTTATCTTTTACCTATATTAGTGAATATCAATTAGTAAGTACTATCTTTATCAT 3992
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DB 3061 ATAGTTTTTAAATTCAGCTGTATTTTCAAGCAGCTTTCCTTGGAAATCACTGTACTGCG 3120
QY 4112 AATGCCACCTTACTTTGCCATGGAATAATGCAGAGATCAATAGATCAAAAGCTTACTCA 4171
DB 3121 AATGCCACCTTACTTTGCCATGGAATAATGCAGAGATCAATAGATCAAAAGCTTACTCA 3161
QY 4172 ACTTAAACTTTCAAGTCTTTTGCATCTGCATATTGGATTGGACAGCTGTGTGTGATAT 4231
DB 3162 -----AGGCTTTTGGCATCTGCATATTGGATTGGACAGCTGTGTGTGATAT 3209
QY 4232 CCCCTTATTTTATCATCTTATTTTGTATGCTAGGAAGCTTACTGGCATTTTCATATTGG 4291
DB 3210 CCCCTTATTTTATCATCTTATTTTGTATGCTAGGAAGCTTATTGGCATTTTCATATTGG 3269
QY 4292 ATTATATTTTATACGTAAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4351
DB 3270 ATTATATTTTATACGTAAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3329
QY 4352 ATCAGTATTTCTGTTCACTTATTTGCTTCTTTCACCTTTTAAAGAAATTTTAAATACCAA 4411
DB 3330 ATCAGTATTTCTGTTCACTTATTTGCTTCTTTCACCTTTTAAAGAAATTTTAAATACCAA 3389
QY 4412 AGAATTTTGGTCAATTTATCTATTTGCTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4471
DB 3390 AGAATTTTGGTCAATTTATCTTCTGTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3449
QY 4472 AACTTTCTTTATGGGATACACAATTTGCAACTATTTCTTCAATTTGCTTGTGATCATCAT 4531
DB 3450 AACTTTCTTTATGGGATACACAATTTGCAACTATTTCTTCAATTTGCTTGTGATCATCAT 3509
QY 4532 TCAATCTATCCATTTCTAGTGTGCTGATTTCTTTTCAATTTGCTTGTGATCATCAT 4591
DB 3510 TCAATCTATCCATTTCTAGTGTGCTGATTTCTTTTCAATTTGCTTGTGATCATCAT 3569
QY 4592 ACGAAATATGCGACACCTATATCCATGGGATAGGCTTTTCAAGTATTTTCAAGTATTTTCAAGT 4651
DB 3570 ACGAAATATGCGACACCTATATCCATGGGATAGGCTTTTCAAGTATTTTCAAGTATTTTCAAGT 3629
QY 4652 TTAACCTGAGTGTGATCTGATTTTCTTTTCAATTTGCTTCAATTTGCTTCAATTTGCTTCAATTTGCT 4711
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QY 4712 CAGATCAATAAGAAAGATCCCTTTTTCAGAAACCTTTTTCAGAAAGCTTAAATATAGGAA 4771

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QY 5192 TTTTGAATTTATGGAGCTGTCAAAGGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 5251
DB 4170 TTTTGAATTTATGGAGCTGTCAAAGGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 4229
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Db 4830 AGAACAGAGGAGGAGATTAATAGTTGTGGAACTTTAAACAGCACACTTTGGTGGGAACG 4889
QY 5912 AACACAGAGGAGGAGATTAATAGTTGTGGAACTTTAAACAGCACACTTTGGTGGGAACG 5939
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US-09-971-121-3
; Sequence 3, Application US/09971121
; Patent No. US2002011147A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; TITLE OF INVENTION: No. US2002011147A1el Human Transporter Proteins and Polynucleot
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4785
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-971-121-3

Query Match 72.9%; Score 4754.8; DB 9; Length 4785;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 4756; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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QY 1071 AATTACTTAATTAATGAGAACCCAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 1130
Db 61 AATTACTTAATTAATGAGAACCCAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 120
QY 1131 TTTTCTTATTTTGGTTAATTAATAGCATGATGATCCAAATAGAAATATGAGAA 1190
Db 121 TTTTCTTATTTTGGTTAATTAATAGCATGATGATCCAAATAGAAATATGAGAA 180
QY 1191 GTGCCTAATATAGAACTCAATCCTATGGACAAAGTTTACTCTTTCTAATCTAATCTTTGGA 1250
Db 181 GTGCCTAATATAGAACTCAATCCTATGGACAAAGTTTACTCTTTCTAATCTAATCTTTGGA 240
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Db 241 TATCTCCAGTCACTAATTAACAGCAGCATCATGCAAGAGTGTCTACTGATCATCTA 300
QY 1311 CCTGATGTCATTAATCTGAGAAATATACAAATGAAAGAAATGTTAAATCCAGTCTC 1370
Db 301 CCTGATGTCATTAATCTGAGAAATATACAAATGAAAGAAATGTTAAATCCAGTCTC 360
QY 1371 TCTAGCCAGCAACTTTGTAGTGTGTTTTCAGAGACTCCATGCTCTATGACTTCGT 1430
Db 361 TCTAGCCAGCAACTTTGTAGTGTGTTTTCAGAGACTCCATGCTCTATGACTTCGT 420
QY 1431 TTTTCTTCTGATATGATTCAGTATCTTCTAATTTATATGATTCAGAGCTGGCTGTTC 1490
Db 421 TTTTCTTCTGATATGATTCAGTATCTTCTAATTTATATGATTCAGAGCTGGCTGTTC 480
QY 1491 AATCATGTGAGGCTGCTCAGTACTGTCCTCAGGTTTTCAGGTTTTCAGGATCCATA 1550
Db 481 AATCATGTGAGGCTGCTCAGTACTGTCCTCAGGTTTTCAGGTTTTCAGGATCCATA 540

QY 1551 GATGCTGCATATATACAGTTGAAGCAACAAATGTTCTCTTTGGAAGGAGCTGGAGTCAACT 1610
Db 541 GATGCTGCATATATACAGTTGAAGCAACAAATGTTCTCTTTGGAAGGAGCTGGAGTCAACT 600
QY 1611 AAAGCTGTTATTTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGGAGGAGTA 1670
Db 601 AAAGCTGTTATTTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGGAGGAGTA 660
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Db 721 GTAGCAGAAAAGAAAATAAAGAAATTTTAAAGATAAATGGGACTTCATGATACT 780
QY 1791 GCCTTTTGGCTTCTCTGGGTTCTCTATATACAGATTTAAATTTTCTTATGCTCCCTCTT 1850
Db 781 GCCTTTTGGCTTCTCTGGGTTCTCTATATACAGATTTAAATTTTCTTATGCTCCCTCTT 840
QY 1851 ATGGCAGTCAATTCGACAGCTTCTTTGTTATTTCTCAAGTAGACAGCAATTTGTATATT 1910
Db 841 ATGGCAGTCAATTCGACAGCTTCTTTGTTATTTCTCAAGTAGACAGCAATTTGTATATT 900
QY 1911 CTGCTTTTCTCTTATGAGATATCATCTGTATTTTGTCTTTAATGCTGACACCTCTT 1970
Db 901 CTGCTTTTCTCTTATGAGATATCATCTGTATTTTGTCTTTAATGCTGACACCTCTT 960
QY 1971 TTTTAAAAAATCAAAACATGCGGAAATAGTTGAAATTTTGTACTGTGGCTTTTGGATTT 2030
Db 961 TTTTAAAAAATCAAAACATGCGGAAATAGTTGAAATTTTGTACTGTGGCTTTTGGATTT 1020
QY 2031 ATGGCTTATGATAAATCCTCATAGAAAGTTTCCAAATGTTAGTGTGGCTTTTCACT 2090
Db 1021 ATGGCTTATGATAAATCCTCATAGAAAGTTTCCAAATGTTAGTGTGGCTTTTCACT 1080
QY 2091 CTTTCTGCTACTGTACTTTTGTGATTGATTTCACAGGTCATGCTGATTTAGAGATTT 2150
Db 1081 CTTTCTGCTACTGTACTTTTGTGATTGATTTCACAGGTCATGCTGATTTAGAGATTT 1140
QY 2151 AATGAAGTGTCTCAATTTTCAAAATTTGACTGAGGCCCATATCTCTAATTTATTTACAA 2210
Db 1141 AATGAAGTGTCTCAATTTTCAAAATTTGACTGAGGCCCATATCTCTAATTTATTTACAA 1200
QY 2211 ATCATGCTCACACTTTAATAGTATATTTCTGCTCTTGGCTGTCTATCTTGTATCAAGTC 2270
Db 1201 ATCATGCTCACACTTTAATAGTATATTTCTGCTCTTGGCTGTCTATCTTGTATCAAGTC 1260
QY 2271 ATTCAGGGGAAATTTGGCTTACGGAGATCATCTTTATTTTCTGAAGCCTTCATATGG 2330
Db 1261 ATTCAGGGGAAATTTGGCTTACGGAGATCATCTTTATTTTCTGAAGCCTTCATATGG 1320
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Db 1501 TCATTTGACATATATGAGGTCAGATTTCTGCTTACTTGGCCACAGTGGAAACAGGAAAG 1560
QY 2571 AGTCAATTTGAGTAAATTTCTTTGAGCTCTGCGCACCTTCTGATGGTTTGCATCTATA 2630
Db 1561 AGTCAATTTGAGTAAATTTCTTTGAGCTCTGCGCACCTTCTGATGGTTTGCATCTATA 1620
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1741 GCTTCAATCAAGGGATACAGCCCAATATAATACAAAGATGCGAGAGGTTTACTA 1800
1811 GATTTAGACATGACAGACTCAAGAGTAACCAAGCTAAAAAATTAAGTGGTGGTCAAAA 2870
1801 GATTTAGACATGACAGACTCAAGAGTAACCAAGCTAAAAAATTAAGTGGTGGTCAAAA 1860
1871 AGAAAGCTGTCATAGGAATGCTGTTTGGGAACCCAAAGATGCTGCTAGATGAA 2930
1861 AGAAAGCTGTCATAGGAATGCTGTTTGGGAACCCAAAGATGCTGCTAGATGAA 1920
1931 CCAACAGCTGGAATGACCCCTGCTCGACATATTTGATGAAATCTTTTAAAAATACAGA 2990
1921 CCAACAGCTGGAATGACCCCTGCTCGACATATTTGATGAAATCTTTTAAAAATACAGA 1980
1991 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCAATTCATGAGTGAAGCTGACATTTGCA 3050
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RESULT 9

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US-10-108-260A-160
; Sequence 160, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cdna
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; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 160
; LENGTH: 3347
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-108-260A-160
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Query Match 49.9%; Score 3258.2; DB 16; Length 3347;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 3327; Conservative 0; Mismatches 4; Indels 47; Gaps 2;

QY 2999 TCGGGTGACAGTGTTCAGTACTCAATTCATGGATGAAGCTGACATTTCTGCAGATAGGAA 3058
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QY 3059 AGCTGTGATATCAAGGAATGCTGAATGTGTGGTCTTCAATGTTCCTCAAAAGTAA 3118
Db 61 AGCTGTGATATCAAGGAATGCTGAATGTGTGGTCTTCAATGTTCCTCAAAAGTAA 120
QY 3119 ATGGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTTGTGCCACAGATCTCT 3178
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QY 3774 -----GACTCAGATATCAGTGTATTTATAGCTTTTTCACAGCAGACATAA 3822
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QY 3823 TGGTGACCATGATTAAATGACAGTGTATGTCGCTGGCTCCCTCATAGTGGCGCTTAA 3882
Db 3882 TGGTGACCATGATTAAATGACAGTGTATGTCGCTGGCTCCCTCATAGTGGCGCTTAA
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QY 3883 ATGTGATGCAATTCAGAAAAAGGACTATGTTTTTGGAGCTGTTTTCAACAGTACTATGGTTT 3942
Db 901 ATGTGATGCAATTCAGAAAAAGGACTATGTTTTTGGAGCTGTTTTCAACAGTACTATGGTTT 960
QY 3943 ATTCTTTTACTATATTAGTGAATATCATATAGTAATCTACTATCTTTATCATATTTAAATGGA 4002
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Db 1081 AATTGAGCTGATTTTCAAGCAGCTTTGCTTGGAAATCAATGTTTCAATGCCACCTT 1140
QY 4123 ACTTTGCCATGGAAATGCAGAGAATCATAGATCAAGCTTATATCTCAACTTAAACTTT 4182
Db 1141 ACTTTGCCATGGAAATGCAGAGAATCATAT----- 1170
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Db 1230 TTATCATCTTATTTTGTAGTCTAGGAAGCTTACTGGCAATTCATTTATGATTTATTTT 1289
QY 4303 ATACTGTAAGTTCCTGTGCTGGTTTTTGTGCTTATTTGGTTATGTTCCATCAGTTATTC 4362
Db 1290 ATACTGTAAGTTCCTGTGCTGGTTTTTGTGCTTATTTGGTTATGTTCCATCAGTTATTC 1349
QY 4363 TGTTCATTTATTTGCTTCTTCACTTTTAAAGAAATTTTAAATACCAAGAAATTTTGGT 4422
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RESULT 10						
US-10-094-749-984						
/	Sequence 984, Application US/10094749					
/	Publication No. US20030219741AI					
/	GENERAL INFORMATION:					
/	APPLICANT: ISOGAI, TAKAO					
/	APPLICANT: SUGIYAMA, TOMOYASU					
/	APPLICANT: OTSUKI, TETSUJI					
/	APPLICANT: WAKAMATSU, AI					
/	APPLICANT: SATO HIROYUKI					
/	APPLICANT: ISHII, SHIZUKO					
/	APPLICANT: YAWAMOTO, JUN-ICHI					
/	APPLICANT: ISONO, YUUOKO					
/	APPLICANT: HIO, YURI					
/	APPLICANT: OTSUKA, KAORU					
/	APPLICANT: NAGAI, KEIICHI					
/	APPLICANT: IRIE, RYOTARO					
/	APPLICANT: TAMECHIKA, ICHEIRO					
/	APPLICANT: SEKI, NAOHICO					
/	APPLICANT: YOSHIKAWA, TSUTOMU					
/	APPLICANT: OTSUKA, MOTOYUKI					
/	APPLICANT: NAGAHARI, KENJI					
/	APPLICANT: MASUHO, YASUHICO					
/	TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA					
/	FILE REFERENCE: 084335/0160					
/	CURRENT APPLICATION NUMBER: US/10/094,749					
/	CURRENT FILING DATE: 2002-03-12					
/	PRIOR APPLICATION NUMBER: 60/350,435					
/	PRIOR FILING DATE: 2002-01-24					
/	PRIOR APPLICATION NUMBER: JP 2001-328381					
/	PRIOR FILING DATE: 2001-09-14					
/	NUMBER Of SEQ ID NOS: 3381					
/	SOFTWARE: Patentin ver. 2.1					
/	SEQ ID NO 984					
/	LENGTH: 3268					
/	TYPE: DNA					
/	ORGANISM: Homo sapiens					
US-10-094-749-984						
Query Match 48.7%; Score 3178; DB 15; Length 3268;						
Best Local Similarity 98.8%; Pred. No. 0;						
Matches 3224; Conservative 0; Mismatches 6; Indels 33; Gaps 1						
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Qy	3162	TGTGCCACAGAAATCTCTTCTTCACTGGTTAAACAAATATACCTGGAGCTACTTTANTA	3221			

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 Db 1206 AGCTTACTGGCAATTCATTATGATATATTTTATCTGTAAAGTTCCTGTCTGTGTT 1265
 QY 4329 TTTTGGCTTATTTGGTATGTTTCACTAGTATTCCTGTTTCACTTATTTGCTTTTCCACC 4388
 Db 1266 TTTTGGCTTATTTGGTATGTTTCACTAGTATTCCTGTTTCACTTATTTGCTTTTCCACC 1325
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 Db 1386 GCTTGTATTTGCAATCACTGAAATAACTTTCTTTTATTTGGGATACACAATTTGCAACTATTTCTT 1445
 QY 4509 CATTATGCTTTTGTATCATCATTCCTCAATCTATCCACTTCTAGTTGGCTGATTTCTTTTC 4568
 Db 1446 CATTATGCTTTTGTATCATCATTCCTCAATCTATCCACTTCTAGTTGGCTGATTTCTTTTC 1505
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 QY 4629 CTTTCACTAGTGTATATTCGCTTACCTGCAAGTGTGTCTGTGGAATTTCTCTTCAAA 4688
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APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
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CURRENT APPLICATION NUMBER: US/09/822,846
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 98
LENGTH: 3928
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-846-98

Query Match 27.4%; Score 1789.4; DB 10; Length 3928;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1833; Conservative 0; Mismatches 1; Indels 33; Gaps 1;
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QY 3021 CATTTTCATGATGAAGCTGACATTTTCAGATAGGAAGCTGTGATATCACAAGGAATG 3080
DB 1081 CATTTTCATGATGAAGCTGACATTTTCAGATAGGAAGCTGTGATATCACAAGGAATG 1140
QY 3081 CTGAAATGTGTTGTTCTTCAATGTTCTCAAAAGTAAATGGGGATCGGCTACCCGCTG 3140
DB 1141 CTGAAATGTGTTGTTCTTCAATGTTCTCAAAAGTAAATGGGGATCGGCTACCCGCTG 1200
QY 3141 AGCATGTACATAGACAAATATTTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAACAT 3200
DB 1201 AGCATGTACATAGACAAATATTTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAACAT 1260
QY 3201 ATACTGAGGCTACTTTATACACAGAAATGACCAACAACTTGTGTATAGCTTGCCTTTC 3260
DB 1261 ATACTGAGGCTACTTTATACACAGAAATGACCAACAACTTGTGTATAGCTTGCCTTTC 1320
QY 3261 AAGGACATGGACAAATTTTCAG-----GTTTG 3287
DB 1321 AAGGACATGGACAAATTTTCAGAAATTTTCAGAAATGCTTTGATGATGTTTG 1380
QY 3288 TTTTCTGCTCCTAGACAGTCAATTTCAATTTGGGTGCTGATTTCTTATGGTGTTCATGAGC 3347
DB 1381 TTTTCTGCTCCTAGACAGTCAATTTCAATTTGGGTGCTGATTTCTTATGGTGTTCATGAGC 1440
QY 3348 ACTTTTGAAGACGTTATTTTAAAGCTAGAGTTGAAGCAGAAATTTGACCAAGCAGATTAT 3407
DB 1441 ACTTTTGAAGACGTTATTTTAAAGCTAGAGTTGAAGCAGAAATTTGACCAAGCAGATTAT 1500
QY 3408 AGTGTATTACTCAGCAGCCTGAGGAGAAATGGAATTCAAATCTTTTGTATGAAATG 3467
DB 1501 AGTGTATTACTCAGCAGCCTGAGGAGAAATGGAATTCAAATCTTTTGTATGAAATG 1560
QY 3468 GAAACAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTT 3527
DB 1561 GAAACAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTT 1620

QY	3528	TGGAACAAACAGATGATATACAAATAGCAAAAGTTTCATTTCTTTTACCTTGAAACGTAAGT	3587
Db	1631	TGGAACAAACAGATGATATACAAATAGCAAAAGTTTCATTTCTTTTACCTTGAAACGTAAGT	1680
QY	3588	AAATCAGTCAGATCAGTGTCTGCTTTTAAATTTTTTTCAGATTCAGATTTTTTATG	3647
Db	1691	AAATCAGTCAGATCAGTGTCTGCTTTTAAATTTTTTTCAGATTCAGATTTTTTATG	1740
QY	3648	TTTTTGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTA	3707
Db	1741	TTTTTGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTA	1800
QY	3708	TATTTTCTTAAACCTGGAGACAAACCATATAAATACAAAACAGTCGTCTTCTTCAAAAT	3767
Db	1801	TATTTTCTTAAACCTGGAGACAAACCATATAAATACAAAACAGTCGTCTTCTTCAAAAT	1860
QY	3768	TCTGCTG 3774	
Db	1861	TCTGCTG 1867	

RESULT 12

US-10-108-260A-1424

; Sequence 1424, Application US/10108260A

; Publication No. US20040005560A1

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: No. US20040005560Aiel full length cDNA

; FILE REFERENCE: HI-A0106

; CURRENT APPLICATION NUMBER: US/10/108,260A

; CURRENT FILING DATE: 2002-03-27

; NUMBER OF SEQ ID NOS: 5458

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1424

; LENGTH: 1943

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-108-260A-1424

Db	629	CATATCCAGGCCCAATGGTAGGAGGTAGAGAGAAAGCAAAAGGGATTGGCCTCATCC	688
Qy	481	TCTTACAAACGATAGTTCATTTGAATAGAGAGAAAGGTTTTCTGCCTCAGAGTGTGGCT	540
Db	689	TCTTACAAACGATAGTTCATTTGAATAGAGAGAAAGGTTTTCCUGCCTCAGAGTGTGGCT	748
Qy	541	GCATAGCGTTTTGTTACTGTAGTCTGGCCCTGTTACCATGGGATGCTTGCATGTGGGG	600
Db	749	GCATAGCGTTTTGTTACTGTAGTCTGGCCCTGTTACCATGGGATGCTTGCATGTGGGG	808
Qy	601	ATACAGGAGATTTCAGAAAAAGAAAGATTTCGTATTTCTACATTTCTCCCTCAGCAATT	660
Db	809	ATACAGGAGATTTCAGAAAAAGAAAGATTTCGTATTTCTACATTTCTCCCTCAGCAATT	868
Qy	661	AAGACCTCCCTTGGCCATTCTCTAAATCAAGCTAAGCCTTCTTCTGGAGCTGGCTCTGT	720
Db	869	AAGACTTCCCTTGGCCATTCTCTAAATCAAGCTAAGCCTTCTTCTGGAGCTGGCTCTGT	928
Qy	721	GGCGGTTTCGGGAGATACCAAGAGAGAAAGTACCACCTGTGTGATATGGTGGTATTTCAA	780
Db	929	GGCGGTTTCGGGAGATACCAAGAGAGAAAGTACCACCTGTGTGATATGGTGGTATTTCAA	988
Qy	781	ATTCGTGHTACCCCTATTTCACATGCTTGTGTTTACTTTTCAGAGCTGACAGATGCTGCT	840
Db	989	ATTCGTGHTACCCCTATTTCACATGCTTGTGTTTACTTTTCAGAGCTGACAGATGCTGCT	1048
Qy	841	CCATGCAATTCGTCCAGTTTCCTAAGAGAGACAGCTTGGAGTAGTCTTAATCCATCTTAC	900
Db	1049	CCATGCAATTCGTCCAGTTTCCTAAGAGAGACAGCTTGGAGTAGTCTTAATCCATCTTAC	1108
Qy	901	CTGGGACTGAACAGCTGCTTATTTTCCCGTTAAAAATTACATGCAGTTTACTGCGTGGC	960
Db	1109	CTGGGACTGAACAGCTGCTTATTTTCCCGTTAAAAATTACATGCAGTTTACTGCGTGGC	1168
Qy	961	TCCGGTTTGTGTTGTTGTTTTCTCTTAAATAGGTTTATTCAGAAAAATGTCACACTG	1020
Db	1169	TCCGGTTTGTGTTGTTGTTTTCTCTTAAATAGGTTTATTCAGAAAAATGTCACACTG	1228
Qy	1021	CAATTAGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAGAAATTACTTAA	1080
Db	1229	CAATTAGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAGAAATTACTTAA	1288
Qy	1081	TAAATCGAGAACCAAAAGAGTAGTGTTCAGAGAAATCTTTTTCACATATTTTTTTAT	1140
Db	1289	TAAATCGAGAACCAAAAGAGTAGTGTTCAGAGAAATCTTTTTCACATATTTTTTTAT	1348
Qy	1141	TTTGGTTAATTAAATPAGCATGATGCATCCAAATAGAAATATGAAGAAAGTCCCTAATA	1200
Db	1349	TTTGGTTAATTAAATPAGCATGATGCATCCAAATAGAAATATGAAGAAAGTCCCTAATA	1408
Qy	1201	TAGAACTCAATCCTATGGACAGTTTACTCTTTCTAATCTAAATCTTGGATATACTCCAG	1260
Db	1409	TAGAACTCAATCCTATGGACAGTTTACTCTTTCTAATCTAAATCTTGGATATACTCCAG	1468
Qy	1261	TGACTAATATTAAAGCAGCATCATCGAGAAAGTGTCTACTGATCATCTACCTGATGTCA	1320
Db	1469	TGACTAATATTAAAGCAGCATCATCGAGAAAGTGTCTACTGATCATCTACCTGATGTCA	1528
Qy	1321	TAAATCTGAAGAAATACAAATGAAGAAAGAAATGTTAACTCCAGCTCTCTTAAGCCGA	1380
Db	1529	TAAATCTGAAGAAATACAAATGAAGAAAGAAATGTTAACTCCAGCTCTCTTAAGCCGA	1588
Qy	1381	GCAACTTTGAGTGTGGTTTTCAAAGACTCCATGTCTTATGAACCTCGTTTTTTTCCCTG	1440
Db	1589	GCAACTTTGAGTGTGGTTTTCAAAGACTCCATGTCTTATGAACCTCGTTTTTTTCCCTG	1648
Qy	1441	ATATGATTCAGGTATCTTCTATTATATGATTCAGAGCTGGCTGTTCAAAATCATGTG	1500
Db	1649	ATATGATTCAGGTATCTTCTATTATATGATTCAGAGCTGGCTGTTCAAAATCATGTG	1708
Qy	1501	AGGCTGCTCAGTACTGGTCTCTCAGGTTTCACAGTTTTCAGAGCATCCATAGATGCTGCA	1560

Db 1709 AGGCTGCTCAGTACTGCTCCTCAGGTTTACAGTTTACAGCATCCATAGATGCTGCCA 1768
Qy 1561 TTATACAGTTGAAGACCAATGTTTCTTTGGAAGAGCTGGAGTCAACTAAAGCTGTTA 1620
Db 1769 TTATACAGTTGAAGACCAATGTTTCTTTGGAAGAGCTGGAGTCAACTAAAGCTGTTA 1828
Qy 1521 TTATGGAGAACTGCTGTTGTAGAAAATAGATACCTTTCCCGAGGAGTAATTTTAATAT 1680
Db 1829 TTATGGAGAACTGCTGTTGTAGAAAATAGATACCTTTCCCGAGGAGTAATTTTAATAT 1888
Qy 1681 ACCTAGTTATAGCAATTTTACCTTTTGGATACCTTTTGGCAATTCATATCGTAGC 1735
Db 1889 ACCTAGTTATAGCAATTTTACCTTTTGGATACCTTTTGGCAATTCATATCGTAGC 1943

RESULT 13
US-10-204-887-32
; Sequence 32, Application US/10204887
; Publication No. US20030124569A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PANZER, Scott R.
; APPLICANT: SPIRO, Peter A.
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; APPLICANT: D'SA, Steven A.
; APPLICANT: AMSHEY, Stefan
; APPLICANT: DAHL, Christopher R.
; APPLICANT: DAM, Tam C.
; APPLICANT: DANIELS, Susan E.
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; APPLICANT: GREENAWALT, Lila B.
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; APPLICANT: JONES, Anissa L.
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; APPLICANT: RUSSO, Frank D.
; APPLICANT: STOCKDREHER, Theresa K.
; APPLICANT: DAFFO, Abel
; APPLICANT: WRIGHT, Rachel J.
; APPLICANT: YAP, Pierre E.
; APPLICANT: YU, Jimmy Y.
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; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: COHEN, Howard J.
; APPLICANT: HODGSON, David M.
; APPLICANT: LINCOLN, Stephen E.
; TITLE OF INVENTION: SECRETORY MOLECULES
; FILE REFERENCE: PT-1134 PCT
; CURRENT APPLICATION NUMBER: US/10/204,887
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/185,215; 60/185,216; 60/205,232; 60/205,323; 60/205,287;
; 60/205,324; 60/205,286
; PRIOR FILING DATE: 2000-02-24; 2000-02-24; 2000-05-16; 2000-05-17; 2000-05-17;
; 2000-05-17; 2000-05-17
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 1818
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124569A1 LI:445188.1:2000MAY01
US-10-204-887-32

Query Match 26.4%; Score 1722.8; DB 15; Length 1818;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1735; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 1 AAAATGTTGATATTTTCTCTTAGCAGGCTGTCAACAGGTTAGGTTTCAAGGTCATAAGTTT 60
Db 81 AAAATGTTGATATTTTCTCTTAGCAGGCTGTCAACAGGTTAGGTTTCAAGGTCATAAGTTT 140
Qy 61 CTACCCACATTTCTTGAACCTGTAGTTGTCAATTTAGTTTATTTTCAAAAACCTTTTSCAG 120
Db 141 CTACCCACATTTCTTGAACCTGTAGTTGTCAATTTAGTTTATTTTCAAAAACCTTTTSCAG 200
Qy 121 TACCTTTTGGTCTGTCTTGTGTGCTTGTGAGTGAACAGTCTGTGAGTTTGGACAGTGGT 180
Db 201 TACCTTTTGGTCTGTCTTGTGTGCTTGTGAGTGAACAGTCTGTGAGTTTGGACAGTGGT 260
Qy 181 CTGTCTGTAGTTTCAAGCTTTCTCAAGCTTTGTCACTAATAGATTTGATATG 240
Db 261 CTGTCTGTAGTTTCTCAAGCTTTGTCACTAATAGATTTGATATG 320
Qy 241 TCCAGCTTGGGAATTTATTTACAGGAATTTAAACAACTTTTGTAGAGTGTCTTCTCGAGCTC 300
Db 321 TCCAGCTTGGGAATTTATTTACAGGAATTTAAACAACTTTTGTAGAGTGTCTTCTCGAGCTC 380
Qy 301 TCTTTCTATTTGTTCCCTTCTACTTTTGTGCTTCCCTGTGCTGCTGTTTCTATCTCTCC 360
Db 381 TCTTTCTATTTGTTCCCTTCTACTTTTGTGCTTCCCTGTGCTGCTGTTTCTATCTCTCC 440
Qy 361 AGCCAGAGAGTGTGTTTATTTTCTCCATTTGTGTACACACTTGTGAGTGTGCAACAC 420
Db 441 AGCCAGAGAGTGTGTTTATTTTCTCCATTTGTGTACACACTTGTGAGTGTGCAACAC 500
Qy 421 CATATCCAGGGCCCAATGTTAGGAGTAGAGAGAAAGAAAGGATTTGGCTCATTC 480
Db 501 CATATCCAGGGCCCAATGTTAGGAGTAGAGAGAAAGAAAGGATTTGGCTCATTC 560
Qy 481 TCTTACACGATAGTTCCATTTGAATAGAGAGAAAGGATTTTCTCCTCAGAGTGTGGCT 540
Db 561 TCTTACACGATAGTTCCATTTGAATAGAGAGAAAGGATTTTCTCCTCAGAGTGTGGCT 620
Qy 541 GCATAGGCTTTTGTACTGTAGTCTGGCCCTGTTACCATGGATTTGCTGATGCTGCTGGG 600
Db 621 GCATAGGCTTTTGTACTGTAGTCTGGCCCTGTTACCATGGATTTGCTGATGCTGCTGGG 680
Qy 601 ATACAGGAGATTTCAAGAAAGAAAGATTTGCTATTTCTACATTTCTCCTCAGAGATTT 660
Db 681 ATACAGGAGATTTCAAGAAAGAAAGATTTGCTATTTCTACATTTCTCCTCAGAGATTT 740
Qy 661 AAGACTCCCTTGGCCATTTCTCAATTTCAAGCTTAAGCTTCTTCTGAGGCTGCTCTGT 720
Db 741 AAGACTCCCTTGGCCATTTCTCAATTTCAAGCTTAAGCTTCTTCTGAGGCTGCTCTGT 800
Qy 721 GGGCGGTTCCGGAGATACCAAGGAGAAAGATTTGCTATTTCTACATTTCTCCTCAGAGATTT 780
Db 801 GGGCGGTTCCGGAGATACCAAGGAGAAAGATTTGCTATTTCTACATTTCTCCTCAGAGATTT 860
Qy 781 ATCTGGTCTACCTTATTTCAATGCTTGTGTTTACTTTTTCAGAGCTGACAGATTTGCTGT 840
Db 861 ATCTGGTCTACCTTATTTCAATGCTTGTGTTTACTTTTTCAGAGCTGACAGATTTGCTGT 920
Qy 841 CCATGCACTTCTGCTCAGTTTCTAAGAGAGACAGCTTGGAGTATGCTTTAATCCATCTTAC 900
Db 921 CCATGCACTTCTGCTCAGTTTCTAAGAGAGACAGCTTGGAGTATGCTTTAATCCATCTTAC 980
Qy 901 CTGGGACTGAAACAGCTGTTATTTTGGCTTTAAATATACATGAGTTTACTCGGTGGC 960
Db 981 CTGGGACTGAAACAGCTGTTATTTTGGCTTTAAATATACATGAGTTTACTCGGTGGC 1040
Qy 961 TCCGGGTTGTTGTTGTTTCTCT - CTTTAAATAGGTTTATTTTCAAGAAACATCTCCACT 1019
Db 1041 TCCGGGTTGTTGTTGTTTCTCTTTTAAATAGGTTTATTTTCAAGAAACATCTCCACT 1100
Qy 1020 GCAATTAAGGAGGTAGGAGTTTGGAGACAGACACACACTTCTTACTGAAGATTACTTA 1079

Db 1101 GCAATTAGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAGAAATACTTTA 1160
QY 1080 ATTAATGCGAACCAAAAGAGTAGTGTTCAGAAATCTTTTCCACTATTTTCTTTA 1139
Db 1161 ATTAATGCGAACCAAAAGAGTAGTGTTCAGAAATCTTTTCCACTATTTTCTTTA 1220
QY 1140 TTTTGGTTAATTAATTAAGCATGTCATCCAAATAGAAATATAGAAAGTGCTTAAT 1199
Db 1221 TTTTGGTTAATTAATTAAGCATGTCATCCAAATAGAAATATAGAAAGTGCTTAAT 1280
QY 1200 ATAGAACTCAATCCTATGAGCAGATTTACTCTTCTAATCTAATCTTCTGATATACTCCA 1259
Db 1281 ATAGAACTCAATCCTATGAGCAGATTTACTCTTCTAATCTAATCTTCTGATATACTCCA 1340
QY 1260 GTGACTAATTAATCAAGCAGCATCATGAGAAAGTGTCTACTGATCATCTACTGATGTC 1319
Db 1341 GTGACTAATTAATCAAGCAGCATCATGAGAAAGTGTCTACTGATCATCTACTGATGTC 1400
QY 1320 ATAAATCTGAAGATATACAAATGAAAGAAATGTTAAACATCCAGTCTCTTAAGCGG 1379
Db 1401 ATAAATCTGAAGATATACAAATGAAAGAAATGTTAAACATCCAGTCTCTTAAGCGG 1460
QY 1380 AGCAACTTTGTAGTGTGTTTCAAGAGCTCCATGTCCTATGAACTTCGTTTCTTCT 1439
Db 1461 AGCAACTTTGTAGTGTGTTTCAAGAGCTCCATGTCCTATGAACTTCGTTTCTTCT 1520
QY 1440 GATATGATCCAGTATCTTCTAATTAATGAAATCAAGAGTGGTGTTCAAAATCATGT 1499
Db 1521 GATATGATCCAGTATCTTCTAATTAATGAAATCAAGAGTGGTGTTCAAAATCATGT 1580
QY 1500 GAGGCTGCTCAGTACGTCCTCAGGTTTCAAGTTTCAAGATCCATGATCCATGATGTC 1559
Db 1581 GAGGCTGCTCAGTACGTCCTCAGGTTTCAAGTTTCAAGATCCATGATCCATGATGTC 1640
QY 1560 ATTATACAGTTGAAGACCAATGTTCTCTTTTGAAGGAGCTGGAGTCAACTAAAGCTGT 1619
Db 1641 ATTATACAGTTGAAGACCAATGTTCTCTTTTGAAGGAGCTGGAGTCAACTAAAGCTGT 1700
QY 1620 ATTATGCGAGAACTGCTGTTAGAAATAGATACCTTTCCCGAGGAGTAAATTAATA 1679
Db 1701 ATTATGCGAGAACTGCTGTTAGAAATAGATACCTTTCCCGAGGAGTAAATTAATA 1760
QY 1680 TACTAGTTATAGCAATTTTCACTTTTGGATGATCTTTTGGCAATTCATATCGTAGCAG 1737
Db 1761 TACTAGTTATAGCAATTTTCACTTTTGGATGATCTTTTGGCAATTCATATCGTAGCAG 1818

RESULT 14

US-09-822-846-97
; Sequence 97, Application US/09822846
; Publication No. US20030027139A1

GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS

; FILE REFERENCE: GIN 6400
; CURRENT APPLICATION NUMBER: US/09/822,846
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,605
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-822-846-97

Query Match 23.7%; Score 1543.8; DB 10; Length 1548;
Best Local Similarity 99.8%; Pred. No. 5.3e-309;
Matches 1545; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3386 AGAAATTCAGCAAGCAGATTATAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGA 3445
Db 1 AGAAATTCAGCAAGCAGATTATAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGA 60
QY 3446 TTCAAAATCTTTTGTGATGAAATGGAACAGAGCTTTACTTTTCTTCTGAAACCAAGCTTC 3505
Db 61 TTCAAAATCTTTTGTGATGAAATGGAACAGAGCTTTACTTTTCTTCTGAAACCAAGCTTC 120
QY 3506 TCTAGTCAGCACCATGAGCCTTTTGGAAACAGAGATGTATACATAGCAAGATTCATTT 3565
Db 121 TCTAGTCAGCACCATGAGCCTTTTGGAAACAGAGATGTATACATAGCAAGATTCATTT 180
QY 3566 CTTTACCTTCAAAACGTGAAAGTAAATCAGTGAGATCAGTGTCTCTCTCTTCTTAAATTTT 3625
Db 181 CTTTACCTTCAAAACGTGAAAGTAAATCAGTGAGATCAGTGTCTCTCTCTTCTTAAATTTT 240
QY 3626 TTTTACAGTTTCAAGTTTAAATGTTTGGTTTCACTCTTTTAAATGCTGTGTTCTC 3685
Db 241 TTTTACAGTTTCAAGTTTAAATGTTTGGTTTCACTCTTTTAAATGCTGTGTTCTC 300
QY 3686 CATCAAACTTGTTCAGACTTATATTTCTFAAACTGGAGACAAACCAATACAA 3745
Db 301 CATCAAACTTGTTCAGACTTATATTTCTFAAACTGGAGACAAACCAATACAA 360
QY 3746 AACAGTCTCTCTTCAAAATCTCTGACTCAGATATCAGTGATCTTATAGCTTTT 3805
Db 361 AACAGTCTCTCTTCAAAATCTCTGACTCAGATATCAGTGATCTTATAGCTTTT 420
QY 3806 CACAAGCCAGAACATATGTCGACGATGATTAATGACAGTACTATGATCCGTGCTC 3865
Db 421 CACAAGCCAGAACATATGTCGACGATGATTAATGACAGTACTATGATCCGTGCTC 480
QY 3866 CCATAGTGGCTTTTAAATGTGATGCAATTCAGAAAAGGACTATGTTTTCAGCTGTTT 3925
Db 481 CCATAGTGGCTTTTAAATGTGATGCAATTCAGAAAAGGACTATGTTTTCAGCTGTTT 540
QY 3926 CAACAGTACTATGCTTTTATCTTACTATATAGTGAATATCATAGTAACTACTATCT 3985
Db 541 CAACAGTACTATGCTTTTATCTTACTATATAGTGAATATCATAGTAACTACTATCT 600
QY 3986 TTATCATTTAAATGTGACTGAAACCAATCCAGATCTGGAGTACCCCATTTCTTCAAGAAAT 4045
Db 601 TTATCATTTAAATGTGACTGAAACCAATCCAGATCTGGAGTACCCCATTTCTTCAAGAAAT 660
QY 4046 TACTGATATAGTTTAAATGAGTGTATTTTCAAGCAGCTTTCTGTTGGAATCATTTGT 4105
Db 661 TACTGATATAGTTTAAATGAGTGTATTTTCAAGCAGCTTTCTGTTGGAATCATTTGT 720
QY 4106 TACTGCAATGCCACCTTACTTTTCCATGGAATGAGAGATCATAGATCAAGCTTTA 4165
Db 721 TACTGCAATGCCACCTTACTTTTCCATGGAATGAGAGATCATAGATCAAGCTTTA 780
QY 4166 TACTCAACTTAAACTTTCAGGCTTTTGGCACTGTCATATTTGGATGGAAGCTTTGT 4225
Db 781 TACTCAACTTAAACTTTCAGGCTTTTGGCACTGTCATATTTGGATGGAAGCTTTGT 840

QY	5802	TATAGCTTTTCTCAAGCAACATTGGAACAGAGTTTTTTGTAGAACTCACTAAAGAACAGAG	5861
Db	1008	TATAGC-TTTCTCAAGCAACATTGGAACAGAGTTTTTTGTAGAACTCACTAAAGAACAGAG	1066
QY	5862	GAGGAGATAATAGTTGTGGAACCTTTAAACACACACACTTTGGTGGGACGACACACAGAA	5921
Db	1067	GAGGAGATAATAGTTGTGGAACCTTTAAACACACACACTTTGGT-GGAACGACACACAGAA	1125
QY	5922	GATAGAGTAGTATTTTGAATTTGTATTTGTCGGTCTGCTTACTGGGACTTCTTCTTTTT	5981
Db	1126	GATAGAGTAGTATTTTGAATTTGTATTTGTCGGTCTGCTTACTGGGACTTCTTCTTTTT	1185
QY	5982	CACTTAATTTTAACTTTGGTTTAAAGTTTTTTTATTTGGAATGGTAACCTGGAGAACCAAG	6041
Db	1186	CACTTAATTTTAACTTTGGTTTAAAGTTTTTTTATTTGGAATGGTAACCTGGAGAACCAAG	1245
QY	6042	AAGCAGCTTGAATTTTCTTAAGCTCCTTAATTGAATGCTGTTGTTGTTGTTTGGCTT	6101
Db	1246	AAGCAGCTTGAATTTTCTTAAGCTCCTTAATTGAATGCTGTTGTTGTTGTTTGGCTT	1305
QY	6102	TTCTTTAAATAAAACGTATGTATAATTAAAGTCAA	6135
Db	1306	TTCTTTAAATAAAACGTATGTATAATTAAAGTCAA	1339

Search completed: December 4, 2004, 20:32:22
Job time : 2970 secs